

A.

HPIV3 L aa 456 (RSV L aa 521) F→L
AEISYEYTLKHWKEISLIEFRKCFDFDPGEELSIFMKDKA-HPIV2 F460
SAISYENAVDYYQSF~~IGIK~~FNKFIEPQLDEDLTIYMKDKA-HPIV3
SAISYECVDNYSSFIGFKFLKFIEPQLDEDLTIYMKDKA-HPIV1

B.

HPIV3 cp45 L aa 942 Y→H
LLPSQLGGLNYLACSRLFNRN-HPIV2 Y948
LIPASVGGFNYMAMSRCFVRN-HPIV3
LIPANIGGFNYMSTARCFVRN-HPIV1

C.

HPIV3 cp45 L aa 992 L→F
LARKPGKGSWATLAADPYSLN-HPIV2 A998
MNQEPGESSFLDWASDPYSCN-HPIV3
MNQEPGDSSFLDWASDPYSCN-HPIV1

D.

HPIV3 cp45 L aa 1558 T→I
DIITPIHAPYLASLDYVKLSI-HPIV2 L1566
GVLNPIYGPNTASQDQIKLLAL-HPIV3
GVVEPVYGPNLSNQDKILLAI-HPIV1

E.

BPIV3 L aa 1711 T→I
EQLETDIILHSTLTA-HPIV2 S1724
EDNILDNIVKTVNDN-BPIV3
EDNMLDNIVKTVNDN-HPIV3
ADSMLDNITAEVQHN-HPIV1

FIGURE 1

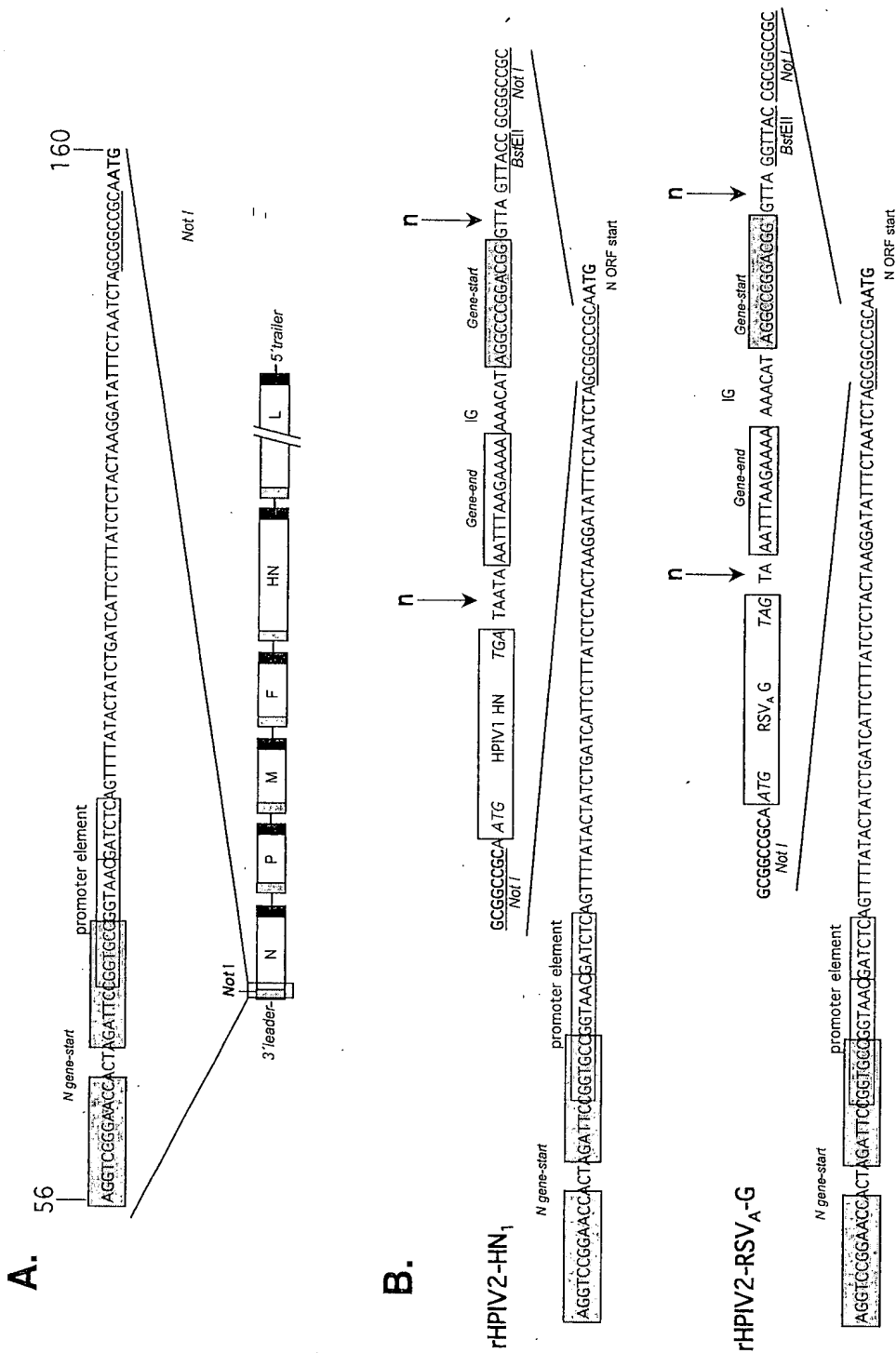


FIGURE 2

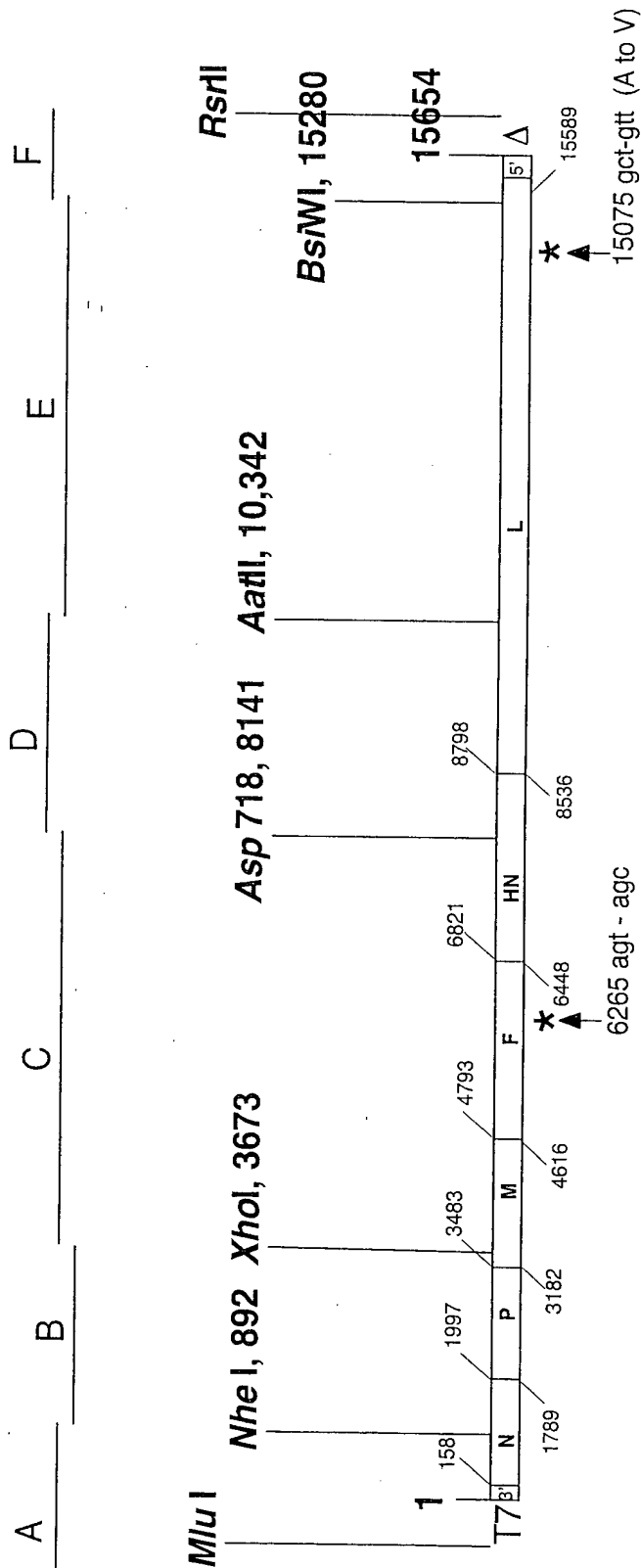


FIGURE 3

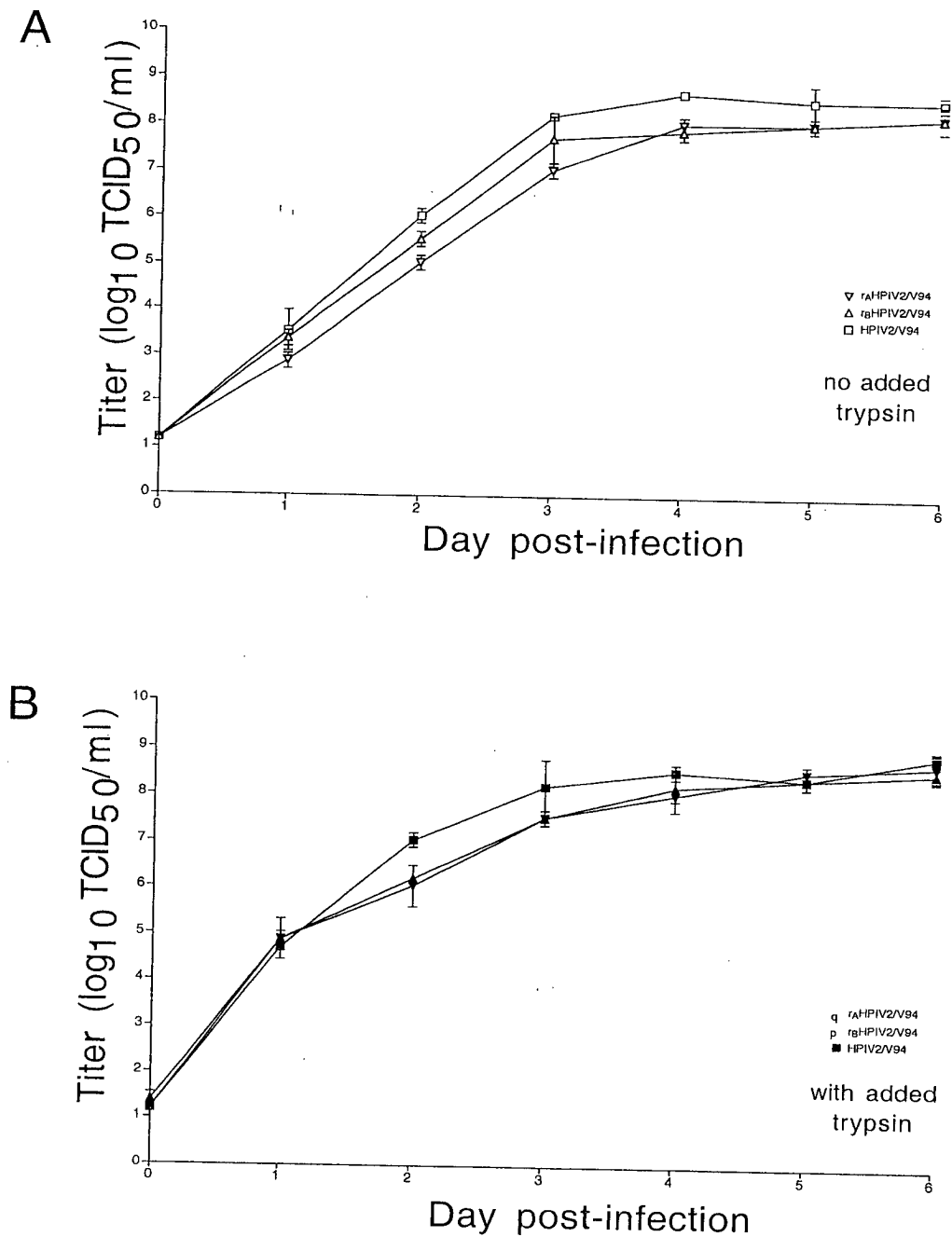


FIGURE 4

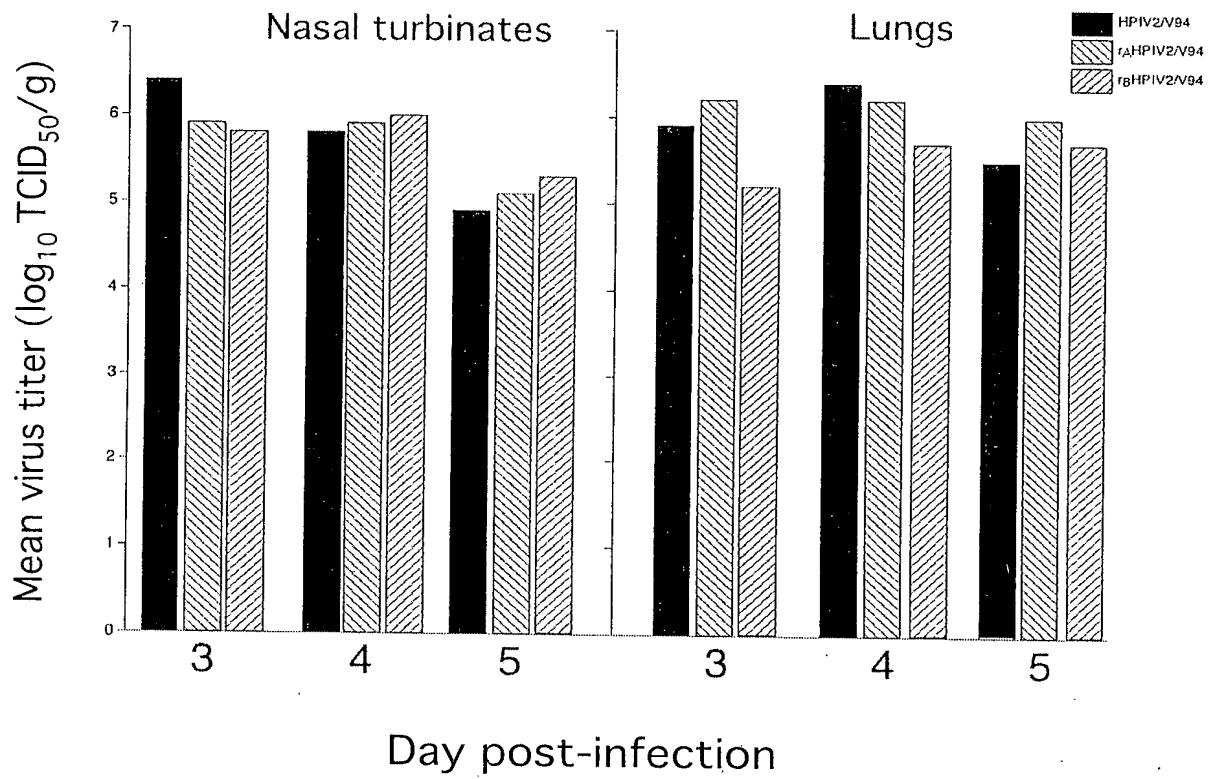


FIGURE 5

A

51	TACGTAGGTCCGGAACCACTAGATT.CGGTGCCGGTAACGATTCCAGTTT	99	Toshiba
51	TACGTAGGTCCGGAACCACTAGATTCCGGTGCCGGTAACGATTCCAGTTT	100	Greer

B

700	ATGACTGCTCCTGATCAACCACCAGTATCAGTAGCAAA...GATGGCTAA	746	Toshiba
701	ATGACTGCTCCTGATCAACCACCAGTATCAGTAGCAAAGCGGATGGCTAA	750	Greer

C

1897	TCTCTCATAATTTAAAGAAAAAATCATAGG.CCGGACGGGTTAGAAATCC	1945	Toshiba
1901	TCTCTCATAATTT.AAGAAAAAATCATAGGCCCGGACGGGTTAGAAATCC	1949	Greer

D

2896	AGTAATTGCCGGTCCAACTAGTGGAGGCTTCACAGCCGAA.CAGGTGATA	2944	Toshiba
2900	AGTAATTGCCGGTCCAACTAGTGGAGGCTTCACAGCCGAAGGCAGTGATA	2949	Greer

E

2945	TTGATTTCAATGGATGAACTAGCTAGACCTACACTCTCATCAACAAAAAG	2994	Toshiba
2950	.TGATTTCAATGGATGAACTAGCTAGACCTACACTCTCATCAACAAAAAG	2998	Greer

F

8595	TTATACGTTTTGGCTGTATTAGAATGTTATAG.ATTCTGCTGTTTTTCCC	8643	Toshiba
8599	TTATACGTTTTGGCTGTATTAGAATGTTATAGCATTCTGCTGTTTTTCCC	8648	Greer

G

9894	TGGGGTCATCCCACTCTTACTGCTGCGCAA...GTGGGTAAAGTGAGAGA	9940	Toshiba
9899	TGGGGTCATCCCACTCTTACTGCTGCGCAAGCTGCAGGTAAAGTGAGAGA	9948	Greer

H

10991	TGATATCTTTATAGTCT...CCAAGGGAGGTATTGAAGGCCTATGTCAGA	11037	Toshiba
10999	TGATATCTTTATAGTCTCTCCCAAGGGAGGTATTGAAGGCCTATGTCAGA	11048	Greer

I

13938	ACAGATATAATTCTTCACTCTACTTTAACTGCTCCTTATGATAATTCAGA	13987	Toshiba
13949	ACAGATATAATTCTTCACTCTACTTTAACTGCTCCTTATGATAATTCAG.	13997	Greer

J

13988	AAACTCTAACAAAGTTCGATTTATCCCTTTTCGACATCTTTCCACATCCAG	14037	Toshiba
13998	AAACTCTAACAAAGTTCGATTTATCCCTT..GACATCTTTCCACATCCAG	14045	Greer

FIGURE 6

A. Site of insertion of oligonucleotides at an EcoRV restriction site in the L polymerase coding sequence

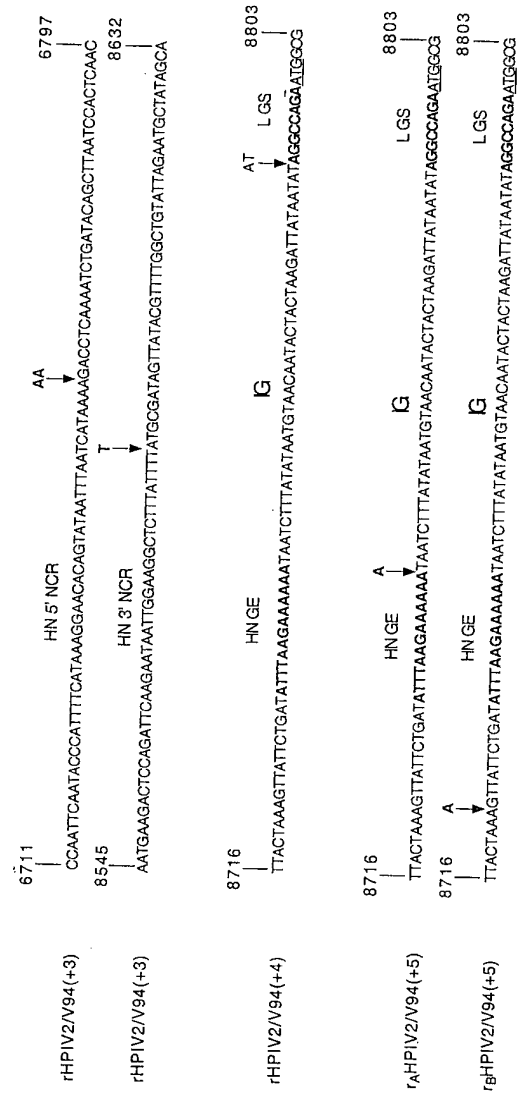
EcoRV ↓
GAT AIC GAG AGG GGT ATC GAT GGC GAA GAA TTA IGA CAA CAG TGA
 HP1V2 nt 15554 ↑
 end of L coding region ↑

B.

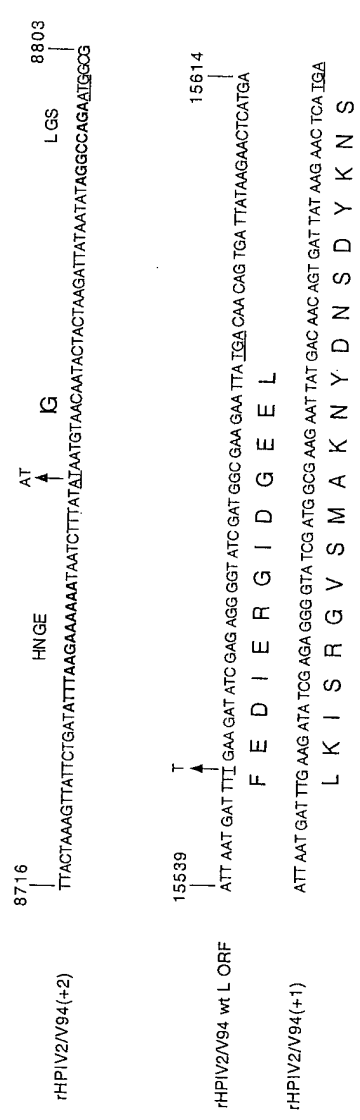
Designation of recovered virus	Oligonucleotide inserted into EcoRV site:	Size of insert	(polyhexameric length; length of cDNA)
rHP1V2/V94 (+6)	<u>ATTGAGAGGGGTATCGATGGCGAAGAATTATGACAACAGTGA</u>	+42 nts	(6n ; 15696 nts)
rHP1V2/V94 (+1)	<u>ATTGAGAGGGGTATCGATGGCGAAGAATTATGACAACAGTGAT</u>	+43 nts	(6n + 1; 15697 nts)
rHP1V2/V94 (+2)	<u>ATTGAGAGGGGTATCGATGGCGAAGAATTATGACAACAGTGATA</u>	+44 nts	(6n + 2; 15698 nts)
rHP1V2/V94 (+3)	<u>ATTGAGAGGGGTATCGATGGCGAAGAATTATGACAACAGTGATAA</u>	+45 nts	(6n + 3; 15699 nts)
rHP1V2/V94 (+4)	<u>ATTGAGAGGGGTATCGATGGCGAAGAATTATGACAACAGTGATAAC</u>	+46 nts	(6n + 4; 15700 nts)
rHP1V2/V94 (+5)	<u>ATTGAGAGGGGTATCGATGGCGAAGAATTATGACAACAGTGATAACT</u>	+47 nts	(6n + 5; 15701 nts)

FIGURE 8

A Genome length modified by nt insertion



B Genome length modified by nt deletion



Human Parainfluenza Virus Type 2 Strain V94 antigenomic sense cDNA Sequence Range: 1 to 15654

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10      20      30      40      50      60      70      80      90      100
ACCAAGGGGA GAATCAGATG GCATCGTTAT ATGACGAATT GCAAAAAAGAT TACGTAGGTC CGGAACCACT AGATTCCGGT GCCGGTAACG ATCTCAGTTT

110     120     130     140     150     160     170     180     190     200
TATACTATCT GATCATTCTT TATCTCTACT AAGGATATTT CTAATCTAAG GTTCAAAATG TCAAGTGTCT TAAAGACATT TGAAGATTG ACTATACAAC

210     220     230     240     250     260     270     280     290     300
AGGAGCTTCA GGAGCAATCT GAAGACACTC CAATACCTCT TGAACAAATC AGACCTACAA TCAGAGTATT TGTCAATCAAT AATAATGATC CTATTGTAAG

310     320     330     340     350     360     370     380     390     400
ATCTAGACTT TTATTCTTTA ATCTACGAAT TATTATGAGT AACACTGCCA GAGAGGGACA TAGAGCTGGT GCTCTCCTCA GTCTTTTATC ACTACCTTCT

410     420     430     440     450     460     470     480     490     500
GCAGCTATGA GTAATCAGAT CAACTAGGCC ATGCATTAC CAGAAGCCAG CATAGATAGA GTAGAAATAA CAGGGTTTGA GAATAATTCA TTCCGAGTTA

510     520     530     540     550     560     570     580     590     600
TTCCAGATGC TCGATCAACT ATGTCCAGAG GAGAAGTGCT GGCCTTCGAA GCATTAGCTG AGGACATTCC TGATACCCTT AATCACCAAA CTCCTATTGT

610     620     630     640     650     660     670     680     690     700
AAATAATGAT GTGGAAGATG ACATATTTGA TGAACAGAG AAATTCCTGG ATGTTTGCTA TAGTGTACTT ATGCAGGCAT GGATAGTAAC ATGCAAGTGC

710     720     730     740     750     760     770     780     790     800
ATGACTGCTC CTGATCAACC ACCAGTATCA GTAGCAAAGC GGATGGCTAA ATATCAACAA CAAGGGAGAA TCAATGCTAG ATATGTACTA CAACCTGAAG

810     820     830     840     850     860     870     880     890     900
CACAAAGACT AATTCAGAAT GCCATCCGCA AGTCAATGGT AGTAAGGCAT TTCATGACCT ATGAGCTTCA ACTTTCACAA TCAAGATCTT TGCTAGCGAA

910     920     930     940     950     960     970     980     990     1000
CCGTTATTAT GCCATGGTGG GAGACATTGG CAAGTATATT GAACACAGCG GAATGGGAGG GTTTTCTTAA AACTTAAAT ATGGACTTGG AACAAAGATG

1010    1020    1030    1040    1050    1060    1070    1080    1090    1100
CCTACATTGG CTCTTGACAG ATTCTCTGGG GAACTCCAGA AATTAAGGC TCTCATGCTA CATTATCAGA GTCTAGGACC CATGGCCAAG TACATGGCTC

1110    1120    1130    1140    1150    1160    1170    1180    1190    1200
TATTAGAATC ACCAAAGCTG ATGGATTGTT TCCCATCTGA ATATCCATTA GTTTATAGCT ATGCAATGGG TATTGGAATC GTCCTTGATA CAAACATGAG

1210    1220    1230    1240    1250    1260    1270    1280    1290    1300
AAACTATGCA TATGGTAGAT CATATCTAAA TCCACAATAT TTTCAGCTAG GGGTAGAAAC AGCAAGGAAA CAGCAAGGAG CTGTTGACAA CAGGACAGCA

1310    1320    1330    1340    1350    1360    1370    1380    1390    1400
GAGGACCTCG GCATGACTGC TGCAGATAAA GCAGACCTCA CTGCAACCAT ATCAAAGCTA TCTTTATCCC AATTACCTAG GGGTAGACAA CCAATATCCG

1410    1420    1430    1440    1450    1460    1470    1480    1490    1500
ACCCATTGCG TGGAGCAAAT GACAGAGAAA CAGGAGGACA AGCAACTGAT ACACCTGTGT ATAACCTCAA TCCAATCAAT AATCGGAGT ATGACAACTA

1510    1520    1530    1540    1550    1560    1570    1580    1590    1600
TGACAGTGAT AGTGAGGACA GAATTGACAA CGATCAAGAT CAGGCTATCA GAGAGAACAG AGGAGAACCT GGACAACCAA ACAACCAGAC AAGCGAAAAAC

1610    1620    1630    1640    1650    1660    1670    1680    1690    1700
CAGCAGAGAG TCAATCTCCC TGTACCGCAA AGAACATCAG GTATGAGTAG TGAAGAGTTC CAACATTCAA TGAATCAGTA CATCCGTGCT ATGCATGAGC

1710    1720    1730    1740    1750    1760    1770    1780    1790    1800
AATACAGAGG CTCCCAGGAT GATGATGCCA ATGATGCCAC AGATGGGAAT GACATTTCAC TTGAGCTAGT TGGAGATTTT GATTCTTAAC TCTCACTTTC

1810    1820    1830    1840    1850    1860    1870    1880    1890    1900
ACATAACCAG ACATACACAT CCACACCACC CAGAGACATA GCTACCATCC ACACACTCAC CCAGACAAAT CAAACTAGAT TCAAATCATT CGGAAACAAT

1910    1920    1930    1940    1950    1960    1970    1980    1990    2000
TCTCCTAGAA TTTAAGAAAA AAACATAGGC CCGGACGGGT TAGAGATCCG GTGCTCGTCT GTGGCCAGAC AACCTCCACA CCAGAGCCAC ACAATCATGG

2010    2020    2030    2040    2050    2060    2070    2080    2090    2100
CCGAGGAACC AACATACACC ACTGAGCAAG TTGATGAATT AATCCATGCT GGACTAGGAA CAGTAGATTT CTCTCTATCT AGACCCATAG ATGCTCAGTC

2110    2120    2130    2140    2150    2160    2170    2180    2190    2200
TTCTTTAGGT AAAGGCAGCA TCCCACCAGG TGTCACGGCT GTTCTAACCA ATGCAGCAGA GGCAAAATCC AAACCAAGTTG CTGCTGGTCC AGTAAAACCC

2210    2220    2230    2240    2250    2260    2270    2280    2290    2300
AGACGGAAGA AAGTGATCAG CAATACCACT CCATACACTA TTGCAGACAA CATCCACCTC GAGAAGCTAC CGATCAACAC TCCAATACCC AATCCATTAC

2310    2320    2330    2340    2350    2360    2370    2380    2390    2400
TTCCACTGGC ACGCCCTCAC GGAAGATGA CAGACATTGA CATTGTCAC TGGGAACATTA CAGAAGGATC ATACAAAGGT GTGGAGCTTG CCAAATTAGG

2410    2420    2430    2440    2450    2460    2470    2480    2490    2500
GAAGCAAACA CTACTACAA GGTTCACCTC GAATGAGCCA GTCTCCTCAG CTGGATCCCG CCAAGACCCC AACTTTAAGA GGGGGGAGC TAATAGAGAA

2510    2520    2530    2540    2550    2560    2570    2580    2590    2600
AGAGCAAGAG GCAACCATAG GAGAGAATGG AGTATTGCAT GGGTCGGAGA TCAGGTCAAA GTCTTCGAGT GGTGTAATCC CAGGTGTGCC CCAGTCACGG

2610    2620    2630    2640    2650    2660    2670    2680    2690    2700
CTTCAGCTCG CAAGTTTACC TGCACATGTG GATCCTGCCC CAGCATCTGC GGAGAATGTG AAGGAGATCA TTGAGCTCTT AAAAGGGCTT GATCTTCGCC

2710    2720    2730    2740    2750    2760    2770    2780    2790    2800
TTCAGACTGT AGAAGGAAAA GTAGATAAAA TTCTTGCAAC CTCTGCAACT ATAATCAATC TTAATAATGA AATGACTAGT CTTAAGGCGA GCGTTGCAAC

2810    2820    2830    2840    2850    2860    2870    2880    2890    2900
TGTGGAAGGT ATGATAACAA CAATTAATAAT CATGGATCCC AGTACACCAA CCAATGTCCC TGTAAGAGAG ATCAGAAAGA GTTTACACAA TGTTCCAGTA

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FIGURE 9A

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2910      2920      2930      2940      2950      2960      2970      2980      2990      3000
GTAATTGCTG GTCCGACTAG TGGAGGCTTC ACAGCCGAAG GCAGTGACAT GATTTC AATG GATGAAGTAG CTAGGCCTAC ACTCTCATCA AAAAAAAGA

3010      3020      3030      3040      3050      3060      3070      3080      3090      3100
TCACACGAAA GCCTGAATCC AAGAAAGATT TAACAGGCAT AAAACTAACC CTGATGCAGC TTGCAAATGA CTGCATCTCG CGTCCAGATA CCAAGACTGA

3110      3120      3130      3140      3150      3160      3170      3180      3190      3200
GTTTGTGACT AAGATTCAAG CAGCAACCAC AGAATCACAG CTC AACGAAA TCAAACGGTC AATAATACGC TCTGCAATAT AAAATGCGGT GCAATCACAC

3210      3220      3230      3240      3250      3260      3270      3280      3290      3300
AAGAGACATT CAACATGCAT CCGATCAAGA TCCAAACTCC TTCCATCCGA AAACACACTC ACCACTGTCA ACACCAAGAA ACAACTACAG CCGAACCATG

3310      3320      3330      3340      3350      3360      3370      3380      3390      3400
CTCAACCAAA AGACCCAAAC AACATCTCAA ATCGACAGAA GGCTAGACAT GATAAATTTA ATAAAAAATT AAAAGAAGTT AAGTAAATTT TAAAGAACAC

3410      3420      3430      3440      3450      3460      3470      3480      3490      3500
AATAGAGAAA ACCTAGGTCC GAAAGCTTGC CTTTCAGACA GATCCCAAAA TCATAGTTCA AACTTCAAAC ACAGCAGCAG ACATGCCTAT AATATCATT

3510      3520      3530      3540      3550      3560      3570      3580      3590      3600
CCAGCAGATC CAACTTCACC CAGTCAATCC CTTACTCCGT TTCCAATACA ACTTGATACC AAAGATGGCA AGGCAGGGAA ACTCTTTAAA CAGATTAGAA

3610      3620      3630      3640      3650      3660      3670      3680      3690      3700
TTAGGTATCT AAATGAACCT AACTCTCGTC ATACACCAAT AACTTTTCATC AATACGTATG GATTGTGTTA TGCTCGAGAC ACTTCAGGAG GCATTCACAG

3710      3720      3730      3740      3750      3760      3770      3780      3790      3800
CGAGATCAGC AGTGACCTAG CTGCAGGGTC CATAACGGCA TGCATGATGA CACTAGGTCC TGGTCCAAAT ATTCAGAAATG CAAATCTAGT GCTAAGATCC

3810      3820      3830      3840      3850      3860      3870      3880      3890      3900
CTGAATGAAT TCTACGTAAA AGTCAAGAAG ACATCAAGCC AGAGGGAGGA AGCAGTGTTT GAATTAGTTA ACATTCCAAC CTTATTGAGA GAACATGCTC

3910      3920      3930      3940      3950      3960      3970      3980      3990      4000
TTTGCAAACG CAAAACGTTA GTATGCTCTG CAGAAAAATT CCTCAAGAAC CCATCAAAGC TACAAGCTGG ATTTGAATAT GTATACATCC CAACTTTTGT

4010      4020      4030      4040      4050      4060      4070      4080      4090      4100
CTCCATTACA TACTCACCAC GAAATCTGAA TTACCAAGTT GCCAGACCTA TCCTTAAGTT CAGATCACGC TTTGTGTATA GCATTCAATT GGAATTAATC

4110      4120      4130      4140      4150      4160      4170      4180      4190      4200
CTGAGATTGC TATGCAAAATC TGACTCCCCT TTGATGAAAT CTTATAATGC AGATCGAACA GGTCGAGGAT GCCTCGCATC AGTCTGGATC CACGTATGTA

4210      4220      4230      4240      4250      4260      4270      4280      4290      4300
ACATTCTGAA AAACAAAAGC ATCAAGCAAC AAGGCAGAGA ATCATATTTC ATAGCTAAGT GCATGAGTAT GCAGCTGCAG GTGTCCATTG CAGATCTTTG

4310      4320      4330      4340      4350      4360      4370      4380      4390      4400
GGGACCAACA ATCATAATTA AATCATTGGG TCACATCCCC AAGACTGCAC TTCCTTTTTT CAGCAAAAGAC GGGATTGCCT GTCATCCACT ACAAGATGTT

4410      4420      4430      4440      4450      4460      4470      4480      4490      4500
TCCCCTACTC TGACAAAATC ACTGTGGTCA GTGGGATGTG AGATAGAATC TGCCAAGTTG ATACTTCAAG AATCTGATAT TAATGAGCTA ATGGGCCACC

4510      4520      4530      4540      4550      4560      4570      4580      4590      4600
AGGACTTGAT TACTGATAAG ATTGCCATTA GATCAGGTCA ACGGACATTT GAGAGGTCCA AATTCAGCCC ATTCAAAAAA TACGCATCAA TTCCAAACTT

4610      4620      4630      4640      4650      4660      4670      4680      4690      4700
AGAAGCCATC AACTGAATGC TCCAGCATCT AGGAATAGAA CAACAACATA GTCATACCAT TATTGACCAT ACAATAATCA ACAATTTTAG CCAACTGATT

4710      4720      4730      4740      4750      4760      4770      4780      4790      4800
ACTAAGATAT TATCATAGGT CCGAACTGAT CAATCTAACA AAAAAACTAA ACATTCAATA ATAAATCAA GTTCAGGCCA AATTATCCAG CCATGCATCA

4810      4820      4830      4840      4850      4860      4870      4880      4890      4900
CCTGCATCCA ATGATAGTAT GCATTTTGT TATGTACACT GGAATTGTAG GTTCAGATGC CATGTGCTGA GATCAACTCC TCAATGTAGG GGTCAATTCAA

4910      4920      4930      4940      4950      4960      4970      4980      4990      5000
TCAAAGATAA GATCACTCAT GTACTACACT GATGGTGGCG CTAGCTTTAT TGTGTGAAA TTACTACCCA ATCTTCCCCC AAGCAATGGA ACATGCAACA

5010      5020      5030      5040      5050      5060      5070      5080      5090      5100
TCACCAGTCT AGATGCATAT AATGTTACCC TATTTAAGTT GCTAACACCC CTGATTGAGA ACCTGAGCAA AATTTCTGCT GTTACAGATA CCAAACCCCG

5110      5120      5130      5140      5150      5160      5170      5180      5190      5200
CCGAGAACGA TTTGCAGGAG TCGTTATTGG GCTTGCTGCA CTAGGAGTAG CTACAGCTGC ACAAATAACC GCAGCTGTAG CAATAGTAAA AGCCAATGCA

5210      5220      5230      5240      5250      5260      5270      5280      5290      5300
AATGCTGCTG CGATAAACAA TCTTGCTACT TCAATTCAAT CCACCAACAA GGCAGTATCC GATGTGATAA CTGCATCAAG AACAAATGCA ACCGCAGTTC

5310      5320      5330      5340      5350      5360      5370      5380      5390      5400
AAGCGATTCA GGATCACATC AATGGAGCCA TTGTCAACGG GATAACATCT GCATCATGCC GTGCCCATGA TGCATAATT GGGTCAATAT TAAATTGTGA

5410      5420      5430      5440      5450      5460      5470      5480      5490      5500
TCTCACTGAG CTTACTACAA TATTTCAATA TCAAATAACA AACCTTGCGC TGACACCACT TTCCATCCAA GCTTTAAGAA TCCTCCTCGG TAGCACCTTG

5510      5520      5530      5540      5550      5560      5570      5580      5590      5600
CCAATTGTCA TTGAATCCAA ACTCAACACA AAACCAACA CAGCAGAGCT GCTCAGTTCC GGACTGTTAA CTGGTCAAAT AATTTCCATT TCCCCAATGT

5610      5620      5630      5640      5650      5660      5670      5680      5690      5700
ACATGCAAAAT GCTAATCAA ATCAATGTTT CGACATTAT AATGCAACCC GGTGCGAAGG TAATTGATCT AATTGCTATC TCTGCAACC ATAAATTACA

5710      5720      5730      5740      5750      5760      5770      5780      5790      5800
AGAAGTAGTT GTACAAGTTC CTAATAGATT TCTAGAATAT GCAAATGAAC TACAAAACCTA CCCAGCCAAT GATTGTGTCG TGACACCAAA CTCTGTATTT
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FIGURE 9B

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5810      5820      5830      5840      5850      5860      5870      5880      5890      5900
TG TAGATACA ATGAGGGTTC CCCGATCCCT GAATCACAAT ATCAATGCTT AAGGGGGAAT CTTAATTCTT GCATTTTAC CCCTATTATC GGAACATTTC

5910      5920      5930      5940      5950      5960      5970      5980      5990      6000
TCAAGCGATT CGCATTTGCC AATGGTGTGC TCTATGCCAA CTGCAAAATCT TTGCTATGTA AGTGTGCCGA CCCTCCCAT GTTGTGTCTC AAGATGACAA

6010      6020      6030      6040      6050      6060      6070      6080      6090      6100
CCAAGGCATC AGCATAATTG ATATTAAGAG GTGCTCTGAG ATGATGCTTG ACACTTTTTC ATTTAGGATC ACATCTACAT TCAATGCTAC ATACGTGACA

6110      6120      6130      6140      6150      6160      6170      6180      6190      6200
GACTTCTCAA TGATTAATGC AAATATTGTA CATCTAAGTC CTCTAGACTT GTCAAATCAA ATCAATTCAA TAAACAAATC TCTTAAAGT GCTGAGGATT

6210      6220      6230      6240      6250      6260      6270      6280      6290      6300
GGATTGCAGA TAGCAACTTC TTCGCTAATC AAGCCAGAAC AGCCAAGACA CTTTATTTCAC TAAGTGCAAT CGCATTAATA CTATCAGTGA TTACTTTGGT

6310      6320      6330      6340      6350      6360      6370      6380      6390      6400
TGTTGTGGGA TTGCTGATTG CCTACATCAT CAAGCTGGTT TCTCAAATCC ATCAATTCAG AGCACTAGCT GCTACAACAA TGTTCACAG GGAGAATCCT

6410      6420      6430      6440      6450      6460      6470      6480      6490      6500
GCCGTCTTTT CCAAGAACAA TCATGGAAAC ATATATGGGA TATCTTAAGA ATTCTATCAT AAGTCCATAT ATGTCCATGA TTGACCTTTA AGAGCCAACC

6510      6520      6530      6540      6550      6560      6570      6580      6590      6600
TCCAATGATT ATCCGTTAAA TTCAGATATA ACAATTCAAA AATCAATATT AAGCCTCCAG ATACCAATGA ATATGAATAT ATCTCTTAGA AAACCTGATT

6610      6620      6630      6640      6650      6660      6670      6680      6690      6700
ATTATGTGAT AACATAGTAC AATTTAAGAA AAAACCTAAA ATAAGCAGCA ACCCTTAAGG TGTCGTAACG TCTCGTGACG CCGGGTTTCCG TTCAAACATC

6710      6720      6730      6740      6750      6760      6770      6780      6790      6800
GACCCCTGAC CCAATTCAT ACCCATTTTC ATAAAGGAAC ACAGTATAAT TTAATCATAA AAGACCTCAA AACTCTGATAC AGCTTAATCC ACTCAACATA

6810      6820      6830      6840      6850      6860      6870      6880      6890      6900
TAATTATAAG ACTAATAATA ATGGAAGATT ACAGCAATCT ATCTCTTAAA TCAATTCCTA AAAGGACATG TAGAATCATT TTCCGAAGTG CCACAATTCT

6910      6920      6930      6940      6950      6960      6970      6980      6990      7000
TGGCATATGC ACATTAATTG TGCTATGTTT AAGTATTCTT CATGAGATAA TTCATCTTGA TGTTCTCTCT GGTCTTATGA ATTCTGATGA GTCACAGCAA

7010      7020      7030      7040      7050      7060      7070      7080      7090      7100
GGCATTATTC AGCCTATCAT AGAATCATT AAATCATTTA TTGCTTTGGC CAACCAGATT CTATATAATG TTGCAATAGT AATCTCTCTT AAAATTGACA

7110      7120      7130      7140      7150      7160      7170      7180      7190      7200
GTATCGAAAC TGTAATACTC TCTGCTTTAA AAGATATGCA CACCGGGAGT ATGTCCAAAT CCAACTGCAC GCCAGGAAAT CTGCTTCTGC ATGATGCAGC

7210      7220      7230      7240      7250      7260      7270      7280      7290      7300
ATACATCAAT GGAATAAACA AATTCCTTGT ACTTGAATCA TACAATGGGA CGCCTAAATA TGGACCTCTC CTAATATATC CCAGCTTTAT CCCCTCAGCA

7310      7320      7330      7340      7350      7360      7370      7380      7390      7400
ACATCTCCCC ATGGGTGTAC TAGAATACCA TCATTTTCAC TCATCAAGAC CCATTGGTGT TACACTCACA ATGTAATGCT TGGAGATTGT CTTGATTTC A

7410      7420      7430      7440      7450      7460      7470      7480      7490      7500
CGGCATCTAA CCAGTATTTA TCAATGGGGA TAATACAACA ATCTGCTGCA GGGTTTCCAA TTTTCAGGAC TATGAAAACC ATTTACCTAA GTGATGGAA T

7510      7520      7530      7540      7550      7560      7570      7580      7590      7600
CAATCGCAA AGCTGTTTCA TCACTGCTAT ACCAGGAGGT TGTGTCTTGT ATTGCTATGT AGCTACAAGG TCTGAAAAG AAGATTATGC CACGACTGAT

7610      7620      7630      7640      7650      7660      7670      7680      7690      7700
CTAGCTGAAC TGAGACTTGC TTCTATTAT TATAATGATA CCTTTATTGA AAGAGTCATA TCTCTTCCAA ATACAACAGG GCAGTGGGCC ACAATCAACC

7710      7720      7730      7740      7750      7760      7770      7780      7790      7800
CTGCAGTCGG AAGCGGGATC TATCATCTAG GCTTTATCTT ATTTCTCTGT TATGTTGCTC TCATAAATGG GACTACTTCT TACAATGAGC AGTCCTCAGC

7810      7820      7830      7840      7850      7860      7870      7880      7890      7900
CTATTTTATC CCAAAACATC CCAACATAAC TTGTGCCGGT AACTCCAGCA AACAGGCTGC AATAGCACGG AGTTCCTATG TCATCCGTTA TCACTCAAAC

7910      7920      7930      7940      7950      7960      7970      7980      7990      8000
AGGTTAATTC AGAGTGCTGT TCTTATTGT CCATTGTCTG ACATGCATAC AGAAGAGTGT AATCTAGTTA TGTTTAACA TTCCCAAGTC ATGATGGGTG

8010      8020      8030      8040      8050      8060      8070      8080      8090      8100
CAGAAGGTAG GCTCTATGTT ATTGGTAATA ATTTGTATTA TTATCAACGC AGTCTCTCTT GGTGGTCTGC ATCGCTCTTT TACAGGATCA ATACAGATTT

8110      8120      8130      8140      8150      8160      8170      8180      8190      8200
TTCTAAAGGA ATTCTCCGA TCATTGAGGC TCAATGGGTA CCGTCCTATC AAGTCTCTCG TCCTGGAGTC ATGCCATGCA ATGCAACAAG TTTTGGCCCT

8210      8220      8230      8240      8250      8260      8270      8280      8290      8300
GCTAATTGCA TCACAGGGT GTACGCAGAT GTGTGGCCGC TTAATGATCC AGAATCATG TCACGTAATG CTCTGAACCC CAACTATCGA TTGCTGGAG

8310      8320      8330      8340      8350      8360      8370      8380      8390      8400
CCTTTCTCAA AAATGAGTCC AACCGAAC TAACCCACATT CTACACTGCA TCGGCTAACT CCTCTTAAA TACTACCGGA TTCAACAACA CCAATCACAA

8410      8420      8430      8440      8450      8460      8470      8480      8490      8500
AGCAGCATAT ACATCTTCAA CCTGCTTTAA AAACACTGGA ACCCAAAAAA TTTATTGTTT AATAATAATT GAAATGGGCT CATCTCTTTT AGGGGAGTTC

8510      8520      8530      8540      8550      8560      8570      8580      8590      8600
CAAATAATAC CATTTTAAAG GGAACATAATG CTTTAATCCT ATTGAATGAA GACTCCAGAT TCAAGAATAA TTGGAAGGCT CTTTATTTTA TGCGATAGTT

8610      8620      8630      8640      8650      8660      8670      8680      8690      8700
ATACGTTTTG GCTGTATTAG AATGCTATAG CATCTGCTG TTTTCCCAT ATGGAAAAAT CCTCAACAC CAACTTAGGT TCAATTTCT CATCATTTAC

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FIGURE 9C

8710 8720 8730 8740 8750 8760 8770 8780 8790 8800
TGTTGTAATT CAATCTTACT AAAGTTATTC TGATATTTAA GAAAAAATAA TCTTTATATA ATGTAACAAT ACTACTAAGA TTATAATATA GGCCAGAATG
8810 8820 8830 8840 8850 8860 8870 8880 8890 8900
GCGGCTCTCT CTGAGATACT CCTTCTGTAA GTCCATTGGA ACTCACCAGT AGTCAAACAC AAACATCATAT ACTACTTATT ACTAGGGCAC TTCCCGCATG
8910 8920 8930 8940 8950 8960 8970 8980 8990 9000
ATCTTGACAT TTCTGAAATA AGCCCCCTTC ACAATAATGA TTGGGATCAG ATTGCCAGAG AAGAATCCAA TCTTGCTGAA CGACTCGGAG TAGCTAAATC
9010 9020 9030 9040 9050 9060 9070 9080 9090 9100
TGAATTAATT AAACGTGTGC CCGCATTTAG AGCAACCAGA TGGCGTAGTC ATGCAGCCGT CCTTATATGG CCTTCTTGTA TACCATTCTT TGTAAATTC
9110 9120 9130 9140 9150 9160 9170 9180 9190 9200
CTACCCCATC CTAAGCTTCA ACCAATAGAA CAATGGTACA AGTTGATCAA TGCTTCATGC AATACTATAT CTGACTCAAT TGATAGATGT ATGGAGAATA
9210 9220 9230 9240 9250 9260 9270 9280 9290 9300
TTTCTATTAA GCTTACTGGG AAAACAATC TATTCTCTCG ATCCAGAGGA ACTGCAGGCG CAGGTAAAAA CAGTAAATC ACCCTCAATG ATATCCAATC
9310 9320 9330 9340 9350 9360 9370 9380 9390 9400
TATTGGGAA TCAAACAAAT GGCAGCCTAA TGTATCTTTA TGGCTTACAA TTAATACCA AATGCGACAA CTTATAATGC ATCAAAGTTC TCGTCAGCCA
9410 9420 9430 9440 9450 9460 9470 9480 9490 9500
ACTGATTAG TTCACATTGT TGACACACGA TCTGGTCTAA TAGTTATCAC CCCTGAACCT GTTATTGTCT TTGATCGGTT GAATAATGTT TTAATGTATT
9510 9520 9530 9540 9550 9560 9570 9580 9590 9600
TTACATTGA GATGACTTTA ATGGTAAGTG ACATGTTTGA GGGACGGATG AATGTTGCCG CGCTCTGCAC TATTAGTCAT TACTTATCAC CACTAGGGCC
9610 9620 9630 9640 9650 9660 9670 9680 9690 9700
AAGGATAGAT AGATTGTTTT CTATTGTAGA TGAATTAGCA CAACTATTGG GTGACACTGT ATATAAAATT ATTGCATCTC TTGAATCTTT AGTATATGGG
9710 9720 9730 9740 9750 9760 9770 9780 9790 9800
TGCTACAAC TTAAAGATCC AGTGGTTGAA TTAACAGGAT CATTTCATTC CTTTATTACG CAAGAGATTA TAGATATCCT AATTGGGTCA AAAGCCCTTG
9810 9820 9830 9840 9850 9860 9870 9880 9890 9900
ATAAGGATGA ATCAATAACT GTCACATCAC AATTGCTAGA TATATTTTCC AACCTTTCTC CAGATTTAAT CGCTGAGATG TTGTGTCTCA TGAGACTTTG
9910 9920 9930 9940 9950 9960 9970 9980 9990 10000
GGGTATCCC ACTCTTACTG CTGCGCAAGC TGCAGGTAAA GTGAGAGAAAT CTATGTGTGC AGGTAAGTTA CTTGATTTCC CTACAATAAT GAAAACCTCTT
10010 10020 10030 10040 10050 10060 10070 10080 10090 10100
GCTTTTTTCC ACACAATTTT AATCAATGGT TATCGTAGAA AGAAGAATGG AATGTGGCCT CCACCTTATAC TTCCTAAAAA TGCATCAAAA AGCTTAATAG
10110 10120 10130 10140 10150 10160 10170 10180 10190 10200
AGTTTCAACA TGATAATGCT GAAATATCTT ATGAGTATAC ACTCAAGCAT TGGAAAGAAA TCTCTCTCAT AGAATTTAGA AAGTGCTTTG ACTTTGATCC
10210 10220 10230 10240 10250 10260 10270 10280 10290 10300
TGGTGAGGAG CTAAGCATTT TTATGAAAGA CAAGGCAATA AGTGCTCCAA AAAGTGATTG GATGAGTGTA TTCCGTAGAA GTCTAATAAA ACAACGACAT
10310 10320 10330 10340 10350 10360 10370 10380 10390 10400
CAGAGACATC ATATTCCATG GCCCAATCCA TTAAACAGAC GTCTATTACT CAATTTCTTA GAAGATGACA GTTTTGATCC AGTTGCTGAG CTTCATATAG
10410 10420 10430 10440 10450 10460 10470 10480 10490 10500
TTACCAATGG TGAATATCTC CGAGATGACA CATTTTGTGC ATCTTACTCA TTAAGAGAGA AAGAAATAAA ACCAGATGGA AGGATATTTG CTAAGCTTAC
10510 10520 10530 10540 10550 10560 10570 10580 10590 10600
TAATAGAAAG CGGTCTTGTC AAGTAATGTC GGAAGCAATT CTTGCAAAATC ACGCAGGTAC TCTAATGAAG GAAAACGGAG TTGTCTTGAA TCAATTATCT
10610 10620 10630 10640 10650 10660 10670 10680 10690 10700
CTGACTAAAT CATTGCTTAC TATGAGTCAA ATTGGCATAA TATCAGAAAA AGCAAGAGAGA TATACCCGAG ATAACATCTC ATCTCAAGGT TTCCATACAA
10710 10720 10730 10740 10750 10760 10770 10780 10790 10800
TCAAGACTGA CTCAAAAAAT AAGAAGAAAA GCAAAATGTC ATCATCATAC CTCACAGATC CTGATGATAC ATTTGAACCT AGTGCATGTT TTATAACTAC
10810 10820 10830 10840 10850 10860 10870 10880 10890 10900
TGATCTTGCT AAATACTGTC TTCAATGGAG ATATCAGACC ATAATCCATT TTGCTCGAAC ATTAACAGAG ATGTATGGAG TTCCACATTT ATTGATATG
10910 10920 10930 10940 10950 10960 10970 10980 10990 11000
ATTCATCTTC GTTTGATTAG ATCTACATTA TATGTTGGTG ATCCATTCAA TCCTCTGTCG ACAACTGATG CCTTCGATCT AGATAAGTA TTAATGGTG
11010 11020 11030 11040 11050 11060 11070 11080 11090 11100
ATATCTTTAT AGTCTCTCCC AAGGGAGGTA TTGAAGGCCT ATGTCAGAAA ATGTGGACAA TGATCTCTAT TTCTGTGATC ATCCTTTCTT CAGCCGAATC
11110 11120 11130 11140 11150 11160 11170 11180 11190 11200
CAAAACAAGA GTAATGAGCA TGGTTCAAGG AGATAATCAG GCGATTGCAG TTACAACAAG AGTTCCTAGA TCATTGCCTA GTGTTCAAGG AAAGGAGTTA
11210 11220 11230 11240 11250 11260 11270 11280 11290 11300
GCCTACGAG CAAGCAAGTT ATTCTTTGAA AGACTTAGGG CAAATAATTA TGGTTTGGGT CATCAACTAA AGGCTCAAGA GACTATAATA AGTCCACGCT
11310 11320 11330 11340 11350 11360 11370 11380 11390 11400
TCTTCATATA TAGTAAACGG GTATTCTATC AAGGACGTAT ACTAACACAG GCACCTAAAA ATGCTAGCAA GTTATGTCTT ACTGCAGATG TATTAGGTGA
11410 11420 11430 11440 11450 11460 11470 11480 11490 11500
ATGTACTCAG GCTTCTCTGCT CAAATCTGTC TACTACAATC ATGAGATTAA CAGAAATGAG GGTGAGAAA GATACATGTT ATAAGCTTAA TATTATCA
11510 11520 11530 11540 11550 11560 11570 11580 11590 11600
TCTATTCGTC AACTCACATA TGATCTAATA TTTCCCAAT ACTCCATACC AGGTGAAACA ATAAGTGAAA TTTCTTACA GCATCCAGA TTAATCTCAC

FIGURE 9D

11610	11620	11630	11640	11650	11660	11670	11680	11690	11700
GTATTGTTCT	GCTCCCTTCA	CAGCTAGGTG	GTCTTAATTA	CCTCGCATGT	AGCAGATTAT	TTAACCGCAA	TATCGGAGAT	CCCCTTGGA	CAGCCGTGGC
11710	11720	11730	11740	11750	11760	11770	11780	11790	11800
AGACCTCAAG	AGGTTAAATTA	AATGTGGTGC	TCTTGAATCA	TGGATACTGT	ACAATTACT	GGCAAGAAAA	CCAGGGAAAG	GTTCATGGGC	CACCTTAGCA
11810	11820	11830	11840	11850	11860	11870	11880	11890	11900
GCCGATCCAT	ACTCATTGAA	TCAAGAATAT	CTTTATCCTC	CTACTACTAT	ACTTAAAGA	CATACTCAA	ATACTTTAAT	GGAGATATGT	CGGAATCCTA
11910	11920	11930	11940	11950	11960	11970	11980	11990	12000
TGTTAAAGGG	AGTTTTTACA	GATAATGCAA	AAGAGGAGGA	AAATCTCCTT	GCAAAATTTC	TTCTTGATCG	TGATATAGTA	TTGCCAAGAG	TCGCACACAT
12010	12020	12030	12040	12050	12060	12070	12080	12090	12100
TATAATAGAT	CAATCCAGCA	TTGGAAGGAA	GAAACAGATA	CAAGGGTTTT	TTGACACCCAC	AAGGACCATA	ATGAGACGAT	CATTGAGAT	CAAACTACTC
12110	12120	12130	12140	12150	12160	12170	12180	12190	12200
TCAACTAGA	AGACACTTTC	AGTCATAGAA	TATAATACTA	ATTATTATCT	TTATAACTAC	CCTGTCATAC	TTAATCCTTT	ACCTATTCTT	GGATATTTAA
12210	12220	12230	12240	12250	12260	12270	12280	12290	12300
ATTATATTAC	TGACCAAAT	TGCAGTATTG	ATATATCTAG	AAGTTTAAGA	AAATTATCAT	GGTCTTCTTT	ATTGAATGGA	AGAACTTTAG	AAGGATTAGA
12310	12320	12330	12340	12350	12360	12370	12380	12390	12400
AACTCCAGAT	CCAATTGAAG	TTGTCAATGG	TTCCTTGATT	GTAGGTACAG	GAGATTGTGA	CTTTTGATG	CAGGGTGACG	ATAAATTCAC	TTGGTTCTTT
12410	12420	12430	12440	12450	12460	12470	12480	12490	12500
TTACCTATGG	GGATAAATTAT	TGATGGAAAT	CCTGAAACTA	ATCCACCCAT	CAGAGTTCCA	TACATTGGGT	CTAGAACAGA	GGAAAGAAGA	GTTGCATCAA
12510	12520	12530	12540	12550	12560	12570	12580	12590	12600
TGGCATATAT	TAAAGGTGCC	ACACACAGTT	TGAAGGCTGC	TCTTAGAGGC	GCAGGGGTAT	ACATTTGGGC	ATTCGGAGAT	ACAGTAGTGA	ACTGGAATGA
12610	12620	12630	12640	12650	12660	12670	12680	12690	12700
TGCACCTGAT	ATCGCAAATA	CTAGGGTTAA	GATATCCCTA	GAGCAACTTC	AGACTCTTAC	ACCTCTTCCT	ACATCTGCAA	ACATTACACA	TCGTTTAGAT
12710	12720	12730	12740	12750	12760	12770	12780	12790	12800
GATGGAGCCA	CAACACTTAA	ATTCACTCCA	GCTAGTTTCT	ATGCATTTC	TAGTTATACT	CATATATCAA	ATGATCAACA	ATATTAGAA	ATAGATCAGA
12810	12820	12830	12840	12850	12860	12870	12880	12890	12900
GAGTAGTCGA	TTCCAATATT	ATTTATCAAC	AATTAATGAT	AACAGGGCTT	GGGATCATTT	AGACCTACCA	TAACCCACCT	ATCAGGACCT	CTACACAGGA
12910	12920	12930	12940	12950	12960	12970	12980	12990	13000
AATCACCCTC	CATTTCGACA	CTAGCTCATC	TTGTTGTGTT	AGAAGGTGAT	ATGTTTGCTT	TATATGTGAG	AGCAATGGAG	AGGTTCCCTCA	GATCATCTGT
13010	13020	13030	13040	13050	13060	13070	13080	13090	13100
CCCTACACTA	ATTCATTGTT	ATATGATCCT	GATCCACTAG	CAGATTATGA	GATTGCACAT	CTAGATTATC	TCTCCTACCA	AGCTAAATTT	GGAAGTACAG
13110	13120	13130	13140	13150	13160	13170	13180	13190	13200
ATTACTACTC	ACTTACTGAT	AAAATTGATC	TATTGGCACA	TTTAAGTCCA	AAACAAATGA	TAAACTCAAT	AATTGGGTGA	GATGAAACAG	TATCAATGTT
13210	13220	13230	13240	13250	13260	13270	13280	13290	13300
CAATGATGCG	GTTATTCATAT	CTGATTATAC	TAATAACTGG	ATTAGTGAAT	GTTCTTATAC	TAAGATAGAT	TTAGTTTTTA	AATTAAATGGC	ATGGAATTTT
13310	13320	13330	13340	13350	13360	13370	13380	13390	13400
CTTCTTGAGC	TTGCATTCCA	GATGTACTAC	CTAAGAATAT	CATCTTGAC	AAATATATTT	GACTATACCT	ACATGACTTT	ACGCAGGATA	CCCGGAAGTC
13410	13420	13430	13440	13450	13460	13470	13480	13490	13500
CTCTAAATAA	TATTGCAGCT	ACTATTAGCC	ACCCAAATTT	ATTAAGACGT	GCAATGAATC	TTGATATTAT	CACCTCCTATA	CATGCACCGT	ATTTGGCTTC
13510	13520	13530	13540	13550	13560	13570	13580	13590	13600
ATTAGATTAT	GTCAAATTA	GTATTGATGC	AATTCAGTGG	GGGGTTAAAC	AAGTTCCTGC	TGATTATCA	AATGGAATTG	ATCTTGAAAT	CTTGATTCTT
13610	13620	13630	13640	13650	13660	13670	13680	13690	13700
TCAGAGGATT	CAATGGAAAT	TAGTGATAGG	GCAATGAATC	TCATTGCTAG	AAAACCTAAT	CTCCTTGAC	TTGTTAAAGG	TGAGAAGTAT	ACATTTCCAA
13710	13720	13730	13740	13750	13760	13770	13780	13790	13800
AAATTAAGG	GATGCCACCA	GAGGAAAGT	GTTTAGTCTT	AACTGAATAC	CTAGCAATGT	GTTATCAGAA	FACTCACCAC	TTAGATCCAG	ATCTTCAAAA
13810	13820	13830	13840	13850	13860	13870	13880	13890	13900
GTATTTATAT	AATCTAATA	ATCCAAATTT	GACTGCATTT	CCCAGTAACA	ACTTCTACTT	AACAAGGAAA	ATCCTTAATC	AAATTAGAGA	ATCAGACGAA
13910	13920	13930	13940	13950	13960	13970	13980	13990	14000
GGACAATATA	TTATCACCTC	ATATTATGAA	TCCTTCGAAC	AATTAGAAAC	AGATATAATT	CTTCACTCTA	CTTTAACTGC	TCCTTATGAT	AATTCAGAAA
14010	14020	14030	14040	14050	14060	14070	14080	14090	14100
CTCTAACAAA	GTTTGATTTA	TCCCTTGACA	TCTTCCACA	TCCAGAATCT	CTCGAGAAAT	ATCCTCTTCC	AGTTGATCAT	GACTCTCAAT	CTGCAATTTT
14110	14120	14130	14140	14150	14160	14170	14180	14190	14200
AACACTAATT	CCAGGCCCTC	CCTCTCATCA	TGTATTACGA	CCACTAGGAG	TGTCATCTAC	AGCTTGGTAT	AAAGGGATAA	GTTATTGCAG	ATACCTGGAA
14210	14220	14230	14240	14250	14260	14270	14280	14290	14300
ACGCAAAAGA	TACAGACTGG	TGATCATCTT	TATTTAGCTG	AAGGAAGCGG	TGCTTCAATG	TCACTTCTAG	AACTCCTATT	TCCAGGAGAT	ACTGCTTATT
14310	14320	14330	14340	14350	14360	14370	14380	14390	14400
ATAATAGTCT	TTTTAGTAGT	GGAGAGAATC	CTCCACAGAG	AAATTATGCT	CCTCTTCCAA	CTCAATTTGT	ACAGAGTGTT	CCATATAAAT	TGTGGCAAGC
14410	14420	14430	14440	14450	14460	14470	14480	14490	14500
TGATCTTGCT	GATGATAGTA	ACTTAATAAA	AGATTTTGTC	CCATTATGGA	ATGGAACCGG	AGCAGTTACA	GACTTATCGA	CAAAGGATGC	AGTTGCATTC

FIGURE 9E

14510	14520	14530	14540	14550	14560	14570	14580	14590	14600
ATAATACATA	AAGTAGGAGC	GGAGAAAGCA	TCCCTTGTTT	ATATAGATCT	CGAATCGACT	GCTAATATAA	ATCAGCAAAC	TCTGTCCAGA	TCCCAGATTG
14610	14620	14630	14640	14650	14660	14670	14680	14690	14700
ATTCGTTAAT	TATAGCAACT	ACTGTTCTTA	AGAGGGGTGG	GATATTAGTT	TACAAAACAT	CATGGCTTCC	GTTTCTAGG	TTTAGTCAAC	TAGCAAGCCT
14710	14720	14730	14740	14750	14760	14770	14780	14790	14800
ACTTTGGTGC	TTTTTGGACC	GGATCCATCT	AATACGTAGT	AGTTATTCTG	ATCCTCACAG	TCATGAGGTT	TATCTTGTAT	GTAGACTTGC	TGCGGATTTT
14810	14820	14830	14840	14850	14860	14870	14880	14890	14900
AGAACTATCG	GTTTCAGTGC	AGCTCTAGTA	ACTGCTACTA	CTCTTCACAA	TGACGGATTC	ACAACAATAC	ATCCTGATGT	TGTTGTAGT	TATTGGCAAC
14910	14920	14930	14940	14950	14960	14970	14980	14990	15000
ACCATCTTGA	GAATGTTGGG	AGAGTCGAAA	AAGTAATTGA	TGAGATACTT	GATGGTTTAG	CCACCAACTT	CTTCGCAGGA	GATAATGGGC	TTATTCTAAG
15010	15020	15030	15040	15050	15060	15070	15080	15090	15100
ATGTGGAGGA	ACTCCCAGCT	CTAGAAAATG	GTTAGAGATT	GATCAGTTAG	CATCATTTGA	TTCAGTTCAA	GATGCTCTAG	TGACACTTAT	CACCATACAC
15110	15120	15130	15140	15150	15160	15170	15180	15190	15200
CTAAAGGAAA	TTATAGAAGT	GCAGTCATCA	CATACAGAGG	ATTATACATC	TCTCCTTTTC	ACACCTTATA	ATATTGGTGC	AGCAGGGAAA	GTAAGAAGTA
15210	15220	15230	15240	15250	15260	15270	15280	15290	15300
TCATCAAATT	AATTCTAGAA	CGATCTTTAA	TGTATACAGT	CCGAAATTGG	TTAGTTTTC	CCAGTTCCAT	CCGGGATTCC	GTACGACAAG	ATCTAGAGTT
15310	15320	15330	15340	15350	15360	15370	15380	15390	15400
AGGGTCATTT	AGATTAATGT	CTATTTTAAG	TGAACAGACA	TTTCTTAAAA	AGACACCCAC	CAAAAAATAC	TTACTTGATC	AGCTTACAAG	GACATATATA
15410	15420	15430	15440	15450	15460	15470	15480	15490	15500
TCAACCTTCT	TTAATTCTCA	CTCAGTCCTC	CCCCTCCACC	GTCCATATCA	AAAACAAATA	TGGAAAGCCT	TAGGTAGTGT	AATATATTGT	TCGGAGACGG
15510	15520	15530	15540	15550	15560	15570	15580	15590	15600
TTGATATACC	TCTAATTAGA	GACATTCAGA	TAGAAGATAT	TAATGATTTT	GAAGATATCG	AGAGGGGTAT	CGATGGCGAA	GAATTATGAC	AACAGTGATT
15610	15620	15630	15640	15650					
ATAAGAAGTC	ATGATAGTTT	TATTTAAGAA	AAACATATTG	ATTTCCCT	TGGT				

Human Parainfluenza Virus Type 2 Strain V98 Antigenomic sense cDNA Sequence Range: 1 to 15654

10	20	30	40	50	60	70	80	90	100
ACCAAGGGGA	GAATTAGATG	GCATCGTTAT	ATGACGAATT	GCAAAAAGAT	TACGTAGGTC	CGGAACCACT	AGATTCCGGT	GCCGGTAACG	ATTCATTTTT
110	120	130	140	150	160	170	180	190	200
TATACTATCT	GATCATTCTC	TATCTCTACT	AAGGATATTT	CTAGTCTAAA	GTTCAAAATG	TCAAGTGTCT	TAAAGACATT	TGAAAGGTTT	ACTATACAAC
210	220	230	240	250	260	270	280	290	300
AAGAGCTTCA	GGAGCAATCT	GATGACACTC	CAGTACCTCT	TGAGACAATC	AAACCTACAA	TAAGGGTATT	TGTCATCAAT	AATAATGATC	CTGCCATAAG
310	320	330	340	350	360	370	380	390	400
GTCTAGACTT	TTATTCTTTA	ATCTACGAAT	TATTATGAGT	AACACCCGAA	GAGAGGGACA	TAGAGCTGGT	GCTCTCCTCA	GTCTCTTATC	ACTACCTTCT
410	420	430	440	450	460	470	480	490	500
GCAGCTATGA	GTAATCACAT	CAAAC TAGCC	ATGCATTAC	CAGAAGCCAG	CATAGATAGA	GTAAGAGATA	CAGGGTTTGA	GAATAATTCA	TTCCGAGTTA
510	520	530	540	550	560	570	580	590	600
TTCCAGATGC	TCGATCAACT	ATGTCCAGAG	GAGAGGTGCT	GGCCTTTGAA	GCATTAGCTG	AAGACATTCC	TGATACCCTT	AATCACCAAA	CTCCATTTGT
610	620	630	640	650	660	670	680	690	700
AAATAATGAT	GTAAGAAGTG	ACATGTTTGA	TGAAACAGAG	AAATCTCTAG	ATGTTTGCTA	CAGTGTACTT	ATGCAGGCAT	GGATAGTAAC	ATGCAAGTGT
710	720	730	740	750	760	770	780	790	800
ATGACTGTCT	CTGATCAGCC	GCCAGTATCA	GAGCAAAAGC	GGATGGCTAA	ATATCAACAA	CAAGGGAGAA	TCAATGCTAG	GTATGTACTA	CAGCCTGAAG
810	820	830	840	850	860	870	880	890	900
CACAAAGACT	AATTCAGAA	GCCATCCGCA	AGTCAATGGT	AGTGAGGCAT	TTTCATGACTT	ATGAGCTTCA	ACTTTCACAA	TCAAGATCTT	TGCTAGCAAA
910	920	930	940	950	960	970	980	990	1000
CCGCTACTAT	GCTATGGTGG	GAGACATTGG	CAAGTACATT	GAACACAGCG	GAATGGGAGG	TTTTTTCTTA	ACACTTAAAT	ATGGACTTGG	AACAAGATGG
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
CCTACATTGG	CTCTTGACG	ATTCTCTGGG	GAATCCAGCA	AATTAAGAAC	TCTCATGCTA	CATTATCAGA	GCCTAGGACC	CATGGCCAA	TACATGGCTC
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
TATTAGAATC	ACCAAAGCTG	ATGGATTGTT	TCCCATCTGA	ATATCCATTA	GTTTATAGTT	ATGCAATGGG	TATTGGAACT	GTCCCTTGATA	CAAATATGAG
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
AAACTATGCA	TATGGTAGAT	CATATTTAAA	TCCGCAATAT	TTTCAGCTAG	GAGTAGAAAC	AGCAAGGAAA	CAGCAGGGAG	CTGTTGACAA	CAGGACAGCA
1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
GAGGACCTCG	GCATGACTGC	TGCAGACAAA	GCAGACCTCA	CTGCAACCAT	ATCAAAGCTA	TCTTTGTCCC	AATTACCTAG	GGGTAGACAA	CCAATATCTG
1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
ACCCATTTCG	TGGAGCAAAT	GACAGAGAAA	TAGGAGGCCA	AGCAAATGAT	ACACCTGTAT	ACAACCTCAA	TCCAATCAAT	ACTCGGAGGT	ATGACAACCTA
1510	1520	1530	1540	1550	1560	1570	1580	1590	1600
TGACAGTGAT	GGTGAGGACA	GAATTGACAA	CGATCAAGAT	CAAGCTATCA	GAGAGAACAG	AGGAGAGCCT	GGACAACATA	ACAACCAGAC	AAGTGACAAC
1610	1620	1630	1640	1650	1660	1670	1680	1690	1700
CAGCAGAGAC	TCAATCTCTC	CATACCAGCA	AGAACATCAG	GTATGAGCAG	TGAAGAGTTC	CAACATTCAA	TGAATCAGTA	CATCCGTGCC	ATGCATGAGC
1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
AATACAGAGG	ACCCAGGAT	GATGATACCA	ATGATGCCGC	AGATGGGAAT	GACATTTCCT	TTGAGCTAGT	TGGGGATTTT	GATTCCCTAAT	TCTCAATGTC
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900
ATACAACCG	ATATACACAT	CCACATCACT	TAAAGATACA	GCTGCCACCC	ACACACTCAT	CCAGACAAAT	CAAACAGAC	TCACATCATT	CAGAAACAAT
1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
TCTCTCATAA	TTTAAGAAAA	AAACATAGGC	CCGACGCGGT	TTAAAATCTG	GTGCTCGTTC	GTGGTCTGAC	AACCTCCAAA	CCAGAATCAC	ACAATTATGG
2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
CCGAGGAACC	AACATACACC	ACTGAGCAAG	TTGATGAAC	AATCCATGCT	GGACTGGGAA	CAGTAGATTT	CTTCCTATCT	AGACCCATAG	ATGCTCAATC
2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
TTCCCTAGGC	AAGGGCAGCA	TCCCACAGG	TGTCACAGCT	GTTCTAAGTA	GTGCAGCAGA	GGCAAAATCC	AAACCAAGTTG	CCGCTGGTCC	AGTGAACCCC
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
AGGCGGAAGA	AAGTGATCAG	CAATGCTACC	CCATACACTG	TTGCAGACAA	TACTCCACCT	GAGAAGCTAC	CAATCAACAC	CCCAATACCC	AATCCATTAC
2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
TTCCACTGGC	ACGCCCCCAA	GGAAAGATGA	CAGACATTGA	CATTGTCACT	GGGACCATT	CAGAGGATC	GTACAAAGGT	GTGGAGCTTG	CTAAATTAGG
2410	2420	2430	2440	2450	2460	2470	2480	2490	2500
GAAGCAAACA	CTACTCACAA	GGTTCACCTC	GAACGAGCCA	GTCTCCTCAG	CTGGATCCGC	CCAAGACCCC	AACCTTAAAG	GGGGGGGAGC	TAATAGAGAA
2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
AGAGCAAGAG	GCAACCATAG	GAGAGAATGG	AGTATTGCA	GGGTCGGAGA	TCAGGTCAAA	GTCTTCGAGT	GGTGAATCC	CAGGTGTGCC	CCAGTCACGG
2610	2620	2630	2640	2650	2660	2670	2680	2690	2700
CCTCAGCTCG	CAAGTTCAAC	TGCACATGCG	GATCCTGCCC	CAGCATCTGC	GGAGAATGTG	AAGGAGATCA	TTGAGCTCTT	AAAGGGGCTT	GATCTTCGCC
2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
TTCAGACTGT	AGAAGGGAAG	GTAAGATAAA	TTCTTGCAAC	TTCCGCAACT	ATAATCAATC	TTAAAAATGA	AATGACTAGT	CTCAAGGCGA	GCGTTGCAAC
2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
TGTGGAAGGT	ATGATAACAA	CAATTAAAA	CATGGATCCC	AGCACACCAA	CCAATGTCCC	TGTAGAGGAG	ATCAGAAAGA	GCTTACACAA	TGCTCCAGTA

FIGURE 10A

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2910      2920      2930      2940      2950      2960      2970      2980      2990      3000
GTAATTGCCG GTCCAAC TAGGAGGCTTC ACAGCCGAAG GCAGTGATAT GATTTC AATG GATGAAGTAG CTAGACCTAC ACTCTCATCA AAAAAAAGA

3010      3020      3030      3040      3050      3060      3070      3080      3090      3100
TCACACGAAA GCCTGAATCC AAGAAAGACT TAACAGGCAC AAAACTAACC TTGATGCAGC TTGCAATGA CTGCATCTCG CGTCCAGATA CCAAGACTGA

3110      3120      3130      3140      3150      3160      3170      3180      3190      3200
GTTCTGTGACT AAGATTCAAG CAGCAACCAC AGAATCACAG CTTAATGAAA TCAAGCGGTC AATAATACGC TCTGCAATAT AAAATGAGGT GCAATCACAC

3210      3220      3230      3240      3250      3260      3270      3280      3290      3300
AAGAGACACT CAACATGCAT CCAATCAAGA TCCAAATTCT GTCCATCCGA AAACACACCC ACAATTGTGA ACACCAAGAA ACAACCACAG CCGAACCATTG

3310      3320      3330      3340      3350      3360      3370      3380      3390      3400
CTTAATCAAA AGATCCAAAC AACATCTCAC ATCGACAGAA GGCTGGACAT GATAAATTTA ATAAAAAAGA AAAAAAAGTC AAGTAAATTT TAAAGGACAC

3410      3420      3430      3440      3450      3460      3470      3480      3490      3500
AATAGAGAAA ATCTAGGTCC GAAAGCTTGC TTCCCGGACA GATCTCAAAA TCATAGTCTA AACCTCAAAC ACAGCAGCAG ACATGCCCAT AATATCATT

3510      3520      3530      3540      3550      3560      3570      3580      3590      3600
CCAGCAGATC CAACTTCACC CAGTCAATCC CTTACTCCGT TTCCAATACA ACTTGACACC AAAGATGGCA AGGCAGGGAA ACTCCTTAAA CAGATTGCGA

3610      3620      3630      3640      3650      3660      3670      3680      3690      3700
TTAGGTATCT AAATGAGCCT AATTCTCGCC ATACACCAAT AACTTTCATC AATACGTATG GATTGTGTTA TGCTCGAGAC ACTTCAGGGG GCATTTCACAG

3710      3720      3730      3740      3750      3760      3770      3780      3790      3800
TGAGCTTAGT AGTGACCTAG CTGCAGGGTC TATAACAGCA TGATGATGA CGCTAGGCCC TGGTCCAAAT ATTGAGAATG CAAATCTAGT GCTAAGATCT

3810      3820      3830      3840      3850      3860      3870      3880      3890      3900
CTGAATGAAT TCTACGTGAA AGTCAAGAAG ACATCAAGCC AGAGAGAGGA AGCAGTGTTC GAATTAGTTA ACATTCCAAC TTTATTGAGA GAACATGCTC

3910      3920      3930      3940      3950      3960      3970      3980      3990      4000
TTTGCAACCG CAAAATGTTA GTTTGCTCTG CAGAAAAGTT CCTCAAGAAC CCGTCAAGAGC TACAAGCTGG ATTTGAGTAT GTATACATAC CAACTTTTGT

4010      4020      4030      4040      4050      4060      4070      4080      4090      4100
CTCCATTACA TACTACCCAC GAAATCTGAA TTACCAAGTT GCCAGACCTA TCCTTAAGTT CAGATCAGCT TTTGTGTATA GCATTCAATT GGAATTAATT

4110      4120      4130      4140      4150      4160      4170      4180      4190      4200
CTGAGATTGC TATGCAAATC TGAATCCCCC TTAATGAAAT CCTACAATGC AGACAAACA GGTGCGGGAT GCCTTGCATC AGTCTGGATC CATGTATGTA

4210      4220      4230      4240      4250      4260      4270      4280      4290      4300
ACATTCTGAA AAACAAAAGC ATCAAGCAAC AAGGCAGAGA ATCATATTTT ATAGCCAAGT GCATGAGCAT GCAGCTGCAG GTGTCCATTG CAGATCTTTG

4310      4320      4330      4340      4350      4360      4370      4380      4390      4400
GGGACCAACA ATCATAATCA AATCATTTGG TCACATCCCC AAGACTGCAC TTCCTTTTTC CAGCAAAGAT GGGATTGCCT GTCATCCATT ACAAGATGTT

4410      4420      4430      4440      4450      4460      4470      4480      4490      4500
TCCCCCACTC TGACAAAATC ACTGTGGTCA GTTGATGTGT AGATAGAATC TGCCAAGTTG ATACTTCAAG AATCTGATCT TAATGAGCTA ATGGGCCACC

4510      4520      4530      4540      4550      4560      4570      4580      4590      4600
AGGACCTTAT CACTGATAAG ATTGCCATCA GATCAGGTCA ACGGACATTT GAGAGGTCCA AATTCAGCCC ATTTAAAAAA TATGCATCAA TTCCAAACTT

4610      4620      4630      4640      4650      4660      4670      4680      4690      4700
GGAAGCCATC AACTGAATGC TCCAGCATCT GAGAATAGAA CCACAATTAA ATCATACTAT TAGTAATAT ACAATAATAA ACAATTTTAG TCAACAGATT

4710      4720      4730      4740      4750      4760      4770      4780      4790      4800
ACCAAGATGT TATCATAGGT CCGAACTGAT CAATCTAACA AAAAAACTAA ACGTTCCATA ATAAATCAAC GTTCAGGTCA AAATACTCAA CCATGCATCA

4810      4820      4830      4840      4850      4860      4870      4880      4890      4900
CCTACATCCA ATGATAGTAT GCATCTTTGT TATGTACACT GGAATTGTAG GTTCAGGTGC CATGTCCGGA GACCAACTAC TTAATATAGG GGTCATTCAA

4910      4920      4930      4940      4950      4960      4970      4980      4990      5000
TCAAAGATAA GATCACTCAT GTACTATACT GATGGTGGTG CTAGCTTTAT TGTGTGTTAA TTGCTACCTA ATCTTCCCCC AAGCAATGGA ACATGCAACA

5010      5020      5030      5040      5050      5060      5070      5080      5090      5100
TTACCACTCT AGATGCATAC AATGTTACCC TATTTAAATT ACTGACACCC CTGATTGAGA ACCTGAGCAA AATCTCCGCT GTTACAGATA CCAAAACCCG

5110      5120      5130      5140      5150      5160      5170      5180      5190      5200
CCAAGAACGA TTTGCAGGAG TCGTTGTTGG ACTTGCTGCA TTAGGAGTAG CCACAGGTGC ACAAATAACC GCAGCTGTAG CAATAGTTAA AGCTAATGCA

5210      5220      5230      5240      5250      5260      5270      5280      5290      5300
AATGTGCGCG CGATTAATAA TCTTGCATCT TCAATTCAAT CAACAACAA GGCAGTATCC GATGTGATAG ATGCATCAAA AACAATTGCA ACTGCAGTTC

5310      5320      5330      5340      5350      5360      5370      5380      5390      5400
AAGCAATCCA GGATCATATC AATGGAGCTA TTGTTAATGG GATAACATCT GCATCATGCC GTGCCCCATGA TGCATCTATT GGGTCAATAT TAAATCTTTA

5410      5420      5430      5440      5450      5460      5470      5480      5490      5500
TCTCACTGAG CTTACCACAA TATTTACAAA TCAAATAACA AACCCTGCGC TGACACCGCT CTCCATCCAA GCTTTAAGAA TTCTCTCTCG TAGCACCTTG

5510      5520      5530      5540      5550      5560      5570      5580      5590      5600
CCAATTGTCA TTGAGTCCAA ACTCAACACA AACCTCAACA CAGCAGAGCT GCTCAGCTCC GGACTGTGTA CTGGTCAAT AATTCAATT TCCCAATGT

5610      5620      5630      5640      5650      5660      5670      5680      5690      5700
ACATGCAAAAT GCTAATTCAA ATCAATGTTC CGACATTAT AATGCAACCC GGTGCGAAGG TAATTGATCT AATTGCTATC TCTGCAAAACC ATAAATGCA

5710      5720      5730      5740      5750      5760      5770      5780      5790      5800
AGAAGTAGTT GTACAAGTTC CGAATAGGAT TCTAGAGTAT GCAATGAAC TACAAAATTA TCCAGCCAAT GACTGTGTTG TGACATCCGA CTCTGTATT

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FIGURE 10B

5810 5820 5830 5840 5850 5860 5870 5880 5890 5900
TG TAGATACA ATGAGGGTTC CCTATCCCT GAATCACAAT ACCAATGCTT GAGGGGGAAT CTTAATTCTT GCACCTTTTAC CCCTATTATC GGGAACTTTT
5910 5920 5930 5940 5950 5960 5970 5980 5990 6000
TTAAGCGATT TGCATTGGCC AATGGTGTGC TCTATGCCAA CTGCAAATCT TTGTGTATGTA AGTGTGCCGA CCCTCCCCAT GTGGTGTCCC AAGATGATAC
6010 6020 6030 6040 6050 6060 6070 6080 6090 6100
CCAAGGCATC AGCATAATTG ATATTAAGAG ATGCTCTGAG ATGATGCTTG ACACCTTCTC ATTTAGGATC ACATCTACGT TCAATGCTAC ATACGTGACA
6110 6120 6130 6140 6150 6160 6170 6180 6190 6200
GACTTCTCAA TGATTAATGC AAATATTGTA CATCTAAGTC CTCTAGATTT GTCAAACCAA ATCAATTCAA TAAACAAATC TCTTAAAGT GCTGAGGATT
6210 6220 6230 6240 6250 6260 6270 6280 6290 6300
GGATTGCAGA TAGCAACTTC TTTGCTAATC AAGCCAGGAC AGCCAAGACA CTTTATTTCAT TAAGTGCAAT AGCATTAAATA CTATCAGTGA TTACCTTGCT
6310 6320 6330 6340 6350 6360 6370 6380 6390 6400
TGTTGTGGGA TTGCTGATTG CCTACATCAT CAAACTAGTT TCCCAATCC ATCAATTTCAG AGCGCTAGCT GCTACAACAA TGTTCACAG GGAATAATCCT
6410 6420 6430 6440 6450 6460 6470 6480 6490 6500
GCCTTCTTTT CCAAGAACAA TCATGGAAAC ATATATGGGA TATCTTAAGA AATCTATCAC AAGTCCATAT ATGTCCACAA TTGATTCTTA AGAACCAACT
6510 6520 6530 6540 6550 6560 6570 6580 6590 6600
TCCAATGATT ATCCCTTTAA CTTAAGTATA ATAGTTTAAA AATTAACATT AAGCCTCCAG ATACCAATGA ATATGAATAT ATCTCTAAGA AAACCTGATT
6610 6620 6630 6640 6650 6660 6670 6680 6690 6700
ATTATGTGAT AGTGTAGTAC AATTTAAGAA AAAACCTAAA ATAAGCAGCA ACCCTTAAGG TGTCGTAACG TCTCGTGACA CTGGTTCAG TTCAAATAATC
6710 6720 6730 6740 6750 6760 6770 6780 6790 6800
GACTTCTAAT CTAATTTAAC ACCCTATTCT ATATAAGAAC ACAGTATAAC TTAATTAGAA AAGACCTCAA AAACCTGACAC AGCTTAATCC ACTCAACATA
6810 6820 6830 6840 6850 6860 6870 6880 6890 6900
TAATTGTAAAG ATTAATAATA ATGGAAGATT ACAGCAATCT ATCTCTTAAA TCAATTCCTA AAAGGACATG TAGAATCATT TTCCGAAGTG CCACAATTCT
6910 6920 6930 6940 6950 6960 6970 6980 6990 7000
TGGAATATGC ACATTGATTG TTCTATGTTC AAGTATTCTT CATGAAATAA TTCATCTTGA TGCTTCCTCT GGTCTCATGA ATTCTGATGA TTCACAGCAA
7010 7020 7030 7040 7050 7060 7070 7080 7090 7100
GGCATTATTC AGCCTATTGT AGAATCATT AAATCATTTGA TTGCTTTGGC TAACCAGATT CTGTACAATG TTGCAATAAT AATTCCTCTT AAAATTGACA
7110 7120 7130 7140 7150 7160 7170 7180 7190 7200
GTATTGAGAC CGTAATACTC TCTGCTTYAA AGGAYATGCA TACTGGGAGC ATGTCCAACA CCAACTGTAC ACCCGGAAT CTGCTTCTGC ATGATGCAGC
7210 7220 7230 7240 7250 7260 7270 7280 7290 7300
ATACATCAAT GGAATAAACA AATTCCTTGT ACTTAATCA TACAATGGTA CGCCTAAATA TGGACCTCTC CTAAATATTC CTAGCTTTAT CCCCTCAGCA
7310 7320 7330 7340 7350 7360 7370 7380 7390 7400
ACATCTCCCC ACGGGTGCAC TAGAATACCA TCATTTTCAC TCAGTAAGAC TCATTGGTGT TACACTCACA ATGTAATACT TGGAGATTGC CTCGATTTC
7410 7420 7430 7440 7450 7460 7470 7480 7490 7500
CGACATCTAA TCAGATTTTA GCAATGGGGA TAATACAACA ATCTGCTGCA GCATTTCCAA TCTTCAGGAC TATGAAAACC ATTTACCTAA GTGATGGAAT
7510 7520 7530 7540 7550 7560 7570 7580 7590 7600
CAATCGAAA AGCTGTTCAG TCACTGCCAT ACCAGGAGGT TGTGTCTGT ACTGCTATGT AGCTACAAGA TCTGAGAAAG AAGATTATGC CACAAGTAT
7610 7620 7630 7640 7650 7660 7670 7680 7690 7700
CTAGCTGAAC TGAGACTTGC TTTCTATTAT TATAATGATA CCTTTGTTGA AAGAGTCATA TCTCTTCCAA ATACAACAGG GCAATGGGCC ACAATCAATC
7710 7720 7730 7740 7750 7760 7770 7780 7790 7800
CTGCAGTTGG AAGCGGGATC TATCATCTAG GCTTTATTTT ATTTCTGTGA TATGGTGGTC TCATAAATGG GACTCCTTCC TACAACGAGC AGTCTCACC
7810 7820 7830 7840 7850 7860 7870 7880 7890 7900
CTATTTTATC CCAACACATC CCAACATAAC CTGTGCCGGA AACTCCAGTG AACGGGCTGC AGCAGCACGG GGTTCCTATG TCATCCGTTA TCATTCAAAAC
7910 7920 7930 7940 7950 7960 7970 7980 7990 8000
AGGTTGATTG AGAGTGCTAT TCTTATTGTC CCATTATCTG ACATGCAAAC AGCAAGGTGT GATCTAGTTA TGTTTAACAA TTCTCAAGTC ATGATGGGTG
8010 8020 8030 8040 8050 8060 8070 8080 8090 8100
CAGAAGGTAG GCTCTATGTT ATTGACAACA ATTTGTATTA TTATCAACGT AGTTCCCTCT GGTGGTCTGC ATCGCTTTTC TACAGGATCA ATACAGATT
8110 8120 8130 8140 8150 8160 8170 8180 8190 8200
CTCTAAAGGA ATTCCTCTTA TCATTGAGGC TCAATGGGTA CCGTCTCTATC AAGTTCCCG CCCTGGAGTC ATGCCATGTA ATGCAACAAG TTTTGGCCCT
8210 8220 8230 8240 8250 8260 8270 8280 8290 8300
GCTAATTGCA TCACAGGAGT GTATGCAGAT GTGTGGCCGC TTAACGATCC AGAAGTCACA TCACAAAATG CTCTGAATCC CAACTATCGA TTTGCTGGAG
8310 8320 8330 8340 8350 8360 8370 8380 8390 8400
CCTTTCTAAA AAATGAGTCC AACCGAACCA ATCCACATTT TTACTCTGCA TCAGCCAACT CCCTACTAAA TACTACCGGA TTCAACAACA CCAATCACAA
8410 8420 8430 8440 8450 8460 8470 8480 8490 8500
AGCAGCATAT ACGTCTTCAA CCTGCTTTAA GAATACTGGA ACTCAGAAGA TTTATTGTTT GATAATAATC GAAATGGGCT CATCTCTTTT AGGGGAGTTC
8510 8520 8530 8540 8550 8560 8570 8580 8590 8600
CAAATAATAC CATTTCTAAG GGAACATAA CCTTAATACT ATTGAATGAA AACTTAAGAT TCAATAATAA TTGAAAGGCT CTCTATCTTA TGTAATAGTT
8610 8620 8630 8640 8650 8660 8670 8680 8690 8700
ATACGTTTTG GCTGTATTAG AATGTTATAG CATTTCTGTG TGTTCCTCAT ATGAAGCAAG CCTCAACAC CGACTTAGGT TCAATTTTCT CATCATTTAC

FIGURE 10C

8710	8720	8730	8740	8750	8760	8770	8780	8790	8800
TGTTGTATATC	CAATCTTACT	AAAGTTATTC	TGATATTTAA	GAATAAATAA	CCTTTATATA	ATATAACAAT	ACTATTAAGA	TTATGATATA	GGCCAGAATG
8810	8820	8830	8840	8850	8860	8870	8880	8890	8900
GCGGCCTCTT	CTGAGATACT	CCTTCTGAA	GTCCACTTGA	ACTCACCAT	AGTCAACAC	AAACTCATAT	ACTACTTATT	ACTAGGGCAC	TTCCCGCATG
8910	8920	8930	8940	8950	8960	8970	8980	8990	9000
ATCTTGACAT	TTCTGAAATA	AGCCCTCTTC	ACAATAATGA	TTGGGATCAA	ATTGCCAGAG	AAGAATCCAA	TCTTGCTGAA	CGACTTGGAG	TAGCTAAATC
9010	9020	9030	9040	9050	9060	9070	9080	9090	9100
TGAATTAAT	AAACGTGTGC	CCGCATTAG	AGCAACTAGA	TGGCGTAGTC	ATGCAGCTGT	CCTTATATGG	CCTTCTTGTA	TACCATTCTT	TGTTAAATTC
9110	9120	9130	9140	9150	9160	9170	9180	9190	9200
CTACCTCATT	CTAAGCTTCA	ACCAATAGAA	CAATGGTACA	AGTTGATACA	TGCTTCATGT	AATACTATAT	CTGACTCAAT	TGATAGATGT	ATGGAGAATA
9210	9220	9230	9240	9250	9260	9270	9280	9290	9300
TTTCTATTAA	GCTTACTGGG	AAAAACAATC	TATTCTCTCG	ATCCAGAGGA	ACTGCAGGTG	CAGGTAAAAA	CAGTAAATAT	ACCCCTCAATG	ATATCCAATC
9310	9320	9330	9340	9350	9360	9370	9380	9390	9400
TATTTTGGGA	TCAACAAGT	GGCAGCTAA	TGTATCTTTA	TGGCTTACAA	TTAAATATCA	AATGCGACAA	CTTATAATGC	ATCAAAGTTC	TCGTAGCCG
9410	9420	9430	9440	9450	9460	9470	9480	9490	9500
ACTGATTAG	TTCACATTGT	TGACACACGA	TCTGGTCTAA	TAGTTATCAC	CCCTGAACCT	GTTATTGTGT	TTGATCGGTT	GAATAGTGT	TTAATGTATT
9510	9520	9530	9540	9550	9560	9570	9580	9590	9600
TTACATTGGA	GATGACTTTA	ATGGTAAGCG	ACATGTTCGA	GGGGAGGATG	AATGTCACTG	CTCTCTGCAC	TATTAGTCAT	TACTTATCTC	CACTAGGGCC
9610	9620	9630	9640	9650	9660	9670	9680	9690	9700
AAGGATCGAT	AGATTGTTTT	CCATTGTAGA	TGAATTAGCA	CAACTATTAG	GTGACACTGT	ATATAAAGTT	ATTGCATCTC	TTGAATCTTT	AGTATATGGG
9710	9720	9730	9740	9750	9760	9770	9780	9790	9800
TGTCTACAAC	TTAAGATCC	AGTAGTGGAA	TTAGCAGGGT	CATTTTCATT	CTTTATTACA	CAAGAGATTA	TAGATATCCT	AATTGGTTCA	AAAGCCCTTG
9810	9820	9830	9840	9850	9860	9870	9880	9890	9900
ATAAGGATGA	ATCAATAACT	GTTACTACAC	AATTGTTAGA	TATATTTTCC	AACCTTCTC	CAGATTAAAT	TGCTGAGATG	TTGTGTCTCA	TGAGACTTTG
9910	9920	9930	9940	9950	9960	9970	9980	9990	10000
GGGTATCCT	ACTCTTACTG	CTGCGCAAGC	TGCAGGTAAA	GTGAGAGAAT	CTATGTGTGC	AGGTAAGTTG	CTTGATTTC	CTACAATAAT	GAAACTCTT
10010	10020	10030	10040	10050	10060	10070	10080	10090	10100
GCTTTTTC	ACACAATTT	AATTAATGGT	TACCGTAGAA	AGAAAAATGG	AATGTGGCCT	CCACTTATAC	TTCTTAAAA	TGCATCAAAA	AGCTTAATAG
10110	10120	10130	10140	10150	10160	10170	10180	10190	10200
AATTTCAACA	TGATAATGCT	GAAATATCTT	ACGAATATAC	ACTCAAGCAT	TGGAAGAGAG	TCTCTCTCAT	AGAATTAGAA	AAGTGTCTTG	ACTTTGATCC
10210	10220	10230	10240	10250	10260	10270	10280	10290	10300
TGGTGAGGAG	CTAAGCATTT	TTATGAAGGA	CAAGGCAATA	AGTGCTCCAA	AAAGTGATTG	GATGAGTGTA	TTTCGTAGAA	GTCTAATAAA	ACAACGACAT
10310	10320	10330	10340	10350	10360	10370	10380	10390	10400
CAGAGACATC	ATATTCCTAT	GCCCAATCCA	TTTAATAGAC	GTCTATTACT	CAATTTCTTA	GAAGATGACA	GTTTGTGACC	AGTTGCTGAG	CTCCAATATG
10410	10420	10430	10440	10450	10460	10470	10480	10490	10500
TTACCACTGG	TGAATACCTC	CAAGATGACA	CATTTTGTGC	ATCTTACTCA	TTAAAAGAGA	AAGAAATAAA	ACCAGATGGA	AGGATATTCT	CTAAGCTTAC
10510	10520	10530	10540	10550	10560	10570	10580	10590	10600
TAATAGAAATG	CGGTCTGTGC	AAGTAATTGC	GGAAGCAATT	CTTGCAAAATC	ATGCAGGTAC	TCTAATGAAG	GAAAACGGAG	TTGTCTTGAA	TCAATTATCA
10610	10620	10630	10640	10650	10660	10670	10680	10690	10700
CTGACCAAGT	CATTGCTTAC	TATGAGTCAA	ATTGGCATAA	TATCAGAAAA	GGCAAGAGAG	TATACGCGAG	ATAACATCTC	ATCTCAAGGT	TTCCATACAA
10710	10720	10730	10740	10750	10760	10770	10780	10790	10800
TCAAGACTGA	CTCTAAAAAT	AAGAGGAAAA	GCAAACTGTC	ATCATCATAC	CTCACAGATC	CTGATGATAC	ATTTGAACTT	AGTGCATGTT	TTATAACTAC
10810	10820	10830	10840	10850	10860	10870	10880	10890	10900
TGATCTTGCT	AAATACTGTC	TTCAATGGAG	ATATCAGACC	ATAATCCATT	TGCTCGAAC	ATTAAACAGA	ATGTATGGAG	TTCCACATTT	ATTTGAATGG
10910	10920	10930	10940	10950	10960	10970	10980	10990	11000
ATTCATCTTC	GTTTAATTAG	GTCTACATTA	TATGTTGGTG	ATCCATTCAA	TCCCCTGCT	GCGACTGATG	CTTTCGATCT	AGATAAAGTA	TTAAATGGTG
11010	11020	11030	11040	11050	11060	11070	11080	11090	11100
ATATCTTTAT	AGTCTCTCCC	AAAGGAGGTA	TTGAAGGCCT	ATGTGAGAAA	ATGTGGACAA	TGATCTCTAT	TTCTGTGATC	ATCCTCTCCT	CAGCCGAATC
11110	11120	11130	11140	11150	11160	11170	11180	11190	11200
CAAAACAAGA	GTAATGAGCA	TGGTTCAAGG	AGATAATCAG	GCAATTGCAG	TTACAACAAG	AGTTCCTAGA	TCATTACCTA	GTATTGAGAA	AAAGGAGTTA
11210	11220	11230	11240	11250	11260	11270	11280	11290	11300
GCCTATGCGG	CAAGCAAGTT	ATTTTGTGAA	AGACTTAGGG	CAAAATTAAT	TGGGTTGGGT	CATCAGCTAA	AGGCTCAAGA	AACTATAATA	AGTTCCACAT
11310	11320	11330	11340	11350	11360	11370	11380	11390	11400
TCTTCATATA	TAGTAAACGG	GATTTTATAT	AAGGACGTAT	ACTAACACAG	GCACTCAAAA	ACGCTAGCAA	GCTATGTCTT	ACTGCGGATG	TATTAGGTGA
11410	11420	11430	11440	11450	11460	11470	11480	11490	11500
ATGTACTCAA	GCTTCTGTGT	CAAAATCTGC	TACTACCATC	ATGAGATTAA	CAGAAAATGG	GGTTGAGAAA	GATACATGTT	ATAAGCTTAA	TATTATATCAG
11510	11520	11530	11540	11550	11560	11570	11580	11590	11600
TCCATTCTGC	AACFCACATA	TGATCTAATA	TTTCCCAAT	ATTCATATACC	AGGTGAAACG	ATAAGTGGGA	TTTCTCTGCA	GCATCCAAGA	CTAATCTCAC

FIGURE 10D

11610 11620 11630 11640 11650 11660 11670 11680 11690 11700
GTATTGTTCT GCTCCCTTCA CAGCTAGGTG GTCTTAATTA CCTCGCATGC AGCAGATTAT TTAACCGCAA TATCGGAGAT CCTCTTGGTA CAGCTGTGGC
11710 11720 11730 11740 11750 11760 11770 11780 11790 11800
GGACCTCAAG AGGTTAATTA AATGTGGTGC TCTTGAATCA TGGATACTGT ACAATTACT AGCAAGAAAA CCAGGGAAG GTTCATGGGC AACTTTAGCA
11810 11820 11830 11840 11850 11860 11870 11880 11890 11900
GCCGATCCGT ACTCATTGAA TCAAGAATAT CTTTATCCTC CTACTACTAT ACTTAAAGA CATACTCAAC ATACTTTAAT GGAGATATGT AGGAATCCCTA
11910 11920 11930 11940 11950 11960 11970 11980 11990 12000
TGTTAAAGGG AGTTTTCACA GATAATGCAA AAGAGGAGGA AAATCTCCTT GCAAAATTC TTCTTGATCG TGATATAGTA TTGCCAAGAG TTGCGCACAT
12010 12020 12030 12040 12050 12060 12070 12080 12090 12100
TATAATAGAT CAATCTAGCA TCGGAAGGAA GAAACAGATA CAAGGATTTT TTGACACCAC AAGGACCATT ATGAGACGAT CATTGGAAT CAAACCACTC
12110 12120 12130 12140 12150 12160 12170 12180 12190 12200
TCAACTAAGA AGACTCTTTC AGTTATAGAA TATAATACAA ATTACTTATC TTATAACTAC CCTGTCTATC TTAATCCTTT ACCTATTCCC GGATATTAA
12210 12220 12230 12240 12250 12260 12270 12280 12290 12300
ATTATATTAC TGACCAACT TGCAGTATTG ATATATCTAG AAGTTAAGA AAATTATCAT GGTCTTCTTT ATTGAATGGA AGAAGTTAG AAGGATTAGA
12310 12320 12330 12340 12350 12360 12370 12380 12390 12400
AATCCAGAT CCAATTGAAG TTGTCAATGG TTCCTTGATT GTAGGTACAG GAGATTGTGA TTTTGTATG CAGGGTGATG ACAAAATTAC TTGGTCTTT
12410 12420 12430 12440 12450 12460 12470 12480 12490 12500
TTACCTATGG GGATAATAT TGATGGAAT CCTGAACTA ATCCACCCAT CAGAGTTCCA TACATTGGGT CTAGAACAGA GGAAAGAAGA GTTGCATCAA
12510 12520 12530 12540 12550 12560 12570 12580 12590 12600
TGGCATATAT TAAAGGTGCC ACACACAGTT TGAAGGCTGC TCTTAGGGGT GCAGGGGTAT ATATTGGGC ATTCGGGGAT ACTATAGTGA ACTGGAATGA
12610 12620 12630 12640 12650 12660 12670 12680 12690 12700
TGCACTTGAT ATTGCAATA CTAGAGTTAA GATATCCCTA GAGCAACTTC AGACTCTCAC ACCTCTTCTT ACATCTGCAA ACATTACACA CCGTTTAGAT
12710 12720 12730 12740 12750 12760 12770 12780 12790 12800
GATGGAGCCA CAACACTTAA ATTCACCTCA GCTAGTTCTT ATGCATTTTC TAGTTATACT CATATATCAA ATGATCAACA ATATTAGAA ATAGATCAGA
12810 12820 12830 12840 12850 12860 12870 12880 12890 12900
GAGTAGTTGA TTCCAATAT ATTTATCAAC AATTAATGAT AACAGGACTT GGGATTATTG AGACCTACCA TAACCCACCT ATAAGAACTT CTACACAAGA
12910 12920 12930 12940 12950 12960 12970 12980 12990 13000
AATCACTCTC CATTTCGACA CTAGCTCATC TTGTGTGTGTT AGAAGTGTAG ATGGCTGCCT TATATGTGAA AGCAATGGAG AGGTTCCTCA GATCACTGTT
13010 13020 13030 13040 13050 13060 13070 13080 13090 13100
CCCTATACTA ATACATTGTT ATATGATCCT GACCCACTAG CAGATTATGA GATTGCACAT CTAGATTACC TCTCCTACCA AGCTAAAATT GGAAGTACAG
13110 13120 13130 13140 13150 13160 13170 13180 13190 13200
ATTACTACTC ACTCACTGAT AAAATTGACC TATTAGCACA TTAACTGCA AAACAAATGA TAAACTCAAT AATTGGGTTA GATGAAACAG TATCGATTGT
13210 13220 13230 13240 13250 13260 13270 13280 13290 13300
CAATGATGCG GTTATCTTAT CTGACTATAC TAATAACTGG ATTAGTGAAT GTTCTTATAC TAAATAGAT CTAGTTTITA AATTAATGGC ATGGAATTTT
13310 13320 13330 13340 13350 13360 13370 13380 13390 13400
CTTCTTGAGC TTGCATTCCA GATGTACTAC TTAAGGATAT CATCTTGGAC AAATATATTT GACTATACCT ACATGACTTT ACGCAGAATA CCCGAACTG
13410 13420 13430 13440 13450 13460 13470 13480 13490 13500
CTCTAAATAA TATTGCAGCT ACTATTAGCC ATCCAAATTT ACTGAGACGT GCAATGAATC TTGATATTAT CACTCCTATA CATGCACCGT ATCTAGCTTC
13510 13520 13530 13540 13550 13560 13570 13580 13590 13600
ATTAGATTAT GTCAAATTAA GTATTGATGC AATTCAGTGG GGAGTTAAAC AAGTCTCTGC TGATTATCA AATGGAATTG ATCTTGAAT CTTGATTCTT
13610 13620 13630 13640 13650 13660 13670 13680 13690 13700
TCAGAGGATT CAATGGAAAT TAGTGATAGG GCAATGAATC TCATTGCTAG AAACTAACT CTCCTTGAC TTGTTAAAGG TGAGAACTAC ACTTTTCCAA
13710 13720 13730 13740 13750 13760 13770 13780 13790 13800
AAATTAAGG GATGCCACCA GAAGAAAAGT GTTAGTCTT AACTGAATAT CTAGCAATGT GTTATCAAAA TACTCACCAC TTAGATCCAG ATCTTCAAAA
13810 13820 13830 13840 13850 13860 13870 13880 13890 13900
GTATTTATAT AATCTAATA ATCCAAATTT GACCGCATTT CCCAGTAACA ACTTCTACTT AACTAGGAAA ATCCTCAATC AAATTAGAGA ATCAGACGAA
13910 13920 13930 13940 13950 13960 13970 13980 13990 14000
GGACAATATA TTATCACCTC ATATTATGAA TCCTTCGAAC AATTAGAAAC AGATATAATT CTTTATCTA CTTTAACTGC TCCTTATGAT AATTCAGAAA
14010 14020 14030 14040 14050 14060 14070 14080 14090 14100
CTCTAACAAA GTTTGATTTA TCCCTTGACA TCTTTCCACA TCCAGAATCT CTCGAGAAAT ATCCTCTTCC AGTTGATCAT GACTCTCAAT CTGCAATTC
14110 14120 14130 14140 14150 14160 14170 14180 14190 14200
AACACTAATT CCAGGCCCTC CTCTCATCA TGTATTACGA CCACTGGGAG TGCTCTCTAC AGCTTGATAT AAAGGGATAA GTTATTGTAG GTATCTAGAA
14210 14220 14230 14240 14250 14260 14270 14280 14290 14300
ACACAAAGA TACAGACTGG TGATCATCTT TATTTAGCTG AAGGAAGCGG CGCTTCAATG TCACTCCTAG AACTCCTATT TCCAGGAGAT ACTGTCTATT
14310 14320 14330 14340 14350 14360 14370 14380 14390 14400
ATAATAGTCT TTTTAGTAGT GGAGAGAATC CTCCACAGAG AAACACAGCC CCTCTTCAA CTCAATTTGT ACAGAGTGT CCATATAAAT TGTGCAAGC
14410 14420 14430 14440 14450 14460 14470 14480 14490 14500
TGATCTTGCT GATGATAGCA ACTTGATAAA AGATTTTGTG CCATTATGGA ATGGAATGG TGCAGTTACA GACTTATCAA CAAAGGATGC AGTTGCATTC

FIGURE 10E

14510	14520	14530	14540	14550	14560	14570	14580	14590	14600
ATAATACATA	AAGTAGGAGC	AGAAAAAGCA	TCTCTTGTCC	ATATAGATCT	CGAATCGACT	GCTAATATAA	ATCAGCAAAC	TCTGTCCAGA	TCCCAGATTC
14610	14620	14630	14640	14650	14660	14670	14680	14690	14700
ATTTCATTAA	TATAGCAACT	ACTGTTCTTA	AGAGGGGTGG	GATATTAAAT	TATAAGACAT	CATGGCTTCC	TTTTTCTAGA	TTTAGTCAAC	TAGCAAGCCT
14710	14720	14730	14740	14750	14760	14770	14780	14790	14800
TCCTTGGTGC	TTTTTTGACC	GGATCCATCT	AATACGTAAG	AGCTATTCTG	ATCCTCACAG	TCATGAGGTT	TATCTTGTAT	GTAGACTTGC	CGCAGATTTT
14810	14820	14830	14840	14850	14860	14870	14880	14890	14900
AGAACTATCG	GTTTCAGTGC	AGCTCTAGTA	ACTGCTACTA	CTCTTCACAA	TGACGGATTC	ACAACAATAC	ATCCTGATGT	TGTTTGTAGT	TATTGGCAAC
14910	14920	14930	14940	14950	14960	14970	14980	14990	15000
ACCATCTTGA	AAATGTTGGG	AGAGTCGGAA	AAGTAATTGA	TGAGATACTT	GATGGTTTAG	CCACCAACTT	CTTTCAGGGA	GATAATGGAC	TTATTCTAAG
15010	15020	15030	15040	15050	15060	15070	15080	15090	15100
ATGTGGAGGA	ACTCCCAGCT	CCAGAAAATG	GTTGGAGATT	GACCAAGTAG	CATCATTTGA	TTTGGTTCAA	GATGCTCTGG	TGACACTTAT	CACTATACAC
15110	15120	15130	15140	15150	15160	15170	15180	15190	15200
CTAAAGGAAA	TTATAGAAGT	GCAATCATCA	CATACAGAAG	ATTATACATC	TCTCCTCTTC	ACACCTTATA	ATATTGGTGC	AGCAGGGAAA	GTTAGAACTA
15210	15220	15230	15240	15250	15260	15270	15280	15290	15300
TCATCAAATT	AATTCTAGAA	CGATCTTTAA	TGTATACAGT	CCGAAATTGG	TTAGTGTTAC	CCAGTTCCAT	CCGGGATTCT	GTACGACAAG	ATTTGGAATT
15310	15320	15330	15340	15350	15360	15370	15380	15390	15400
AGGGTCATTT	AGATTAATGT	CTATTTTAAG	TGAACAGACA	TTTCTTAAAA	AGACACCCAC	AAAAAATAC	TTACTTGATC	AGCTTACAAG	GACATATATA
15410	15420	15430	15440	15450	15460	15470	15480	15490	15500
TCAACCTTCT	TTAACTCTCA	CTCAGTCCTT	CCTCTTCACC	GTCCATATCA	AAAACAAATA	TGGAAAGCCT	TAGGTAGTGT	AATATATTGT	TCGGAGACAG
15510	15520	15530	15540	15550	15560	15570	15580	15590	15600
TTGATATACC	TCTAATTAAA	GACATTCAGA	TAGAAGATAT	TAATGATTTT	GAGGATATCG	AGAGGGGTAT	CGATGGCGAA	GAATTATGAC	AACAATGATT
15610	15620	15630	15640	15650					
ATAAGAAGCT	ATGATAGTTT	TATTTAAGAA	AAACATATTG	ATTTTCCCTT	TGGT				

Human Parainfluenza Virus Type 2 Strain Greer, antigenomic sense cDNA Sequence Range: 1 to 15654

10	20	30	40	50	60	70	80	90	100
ACCAAGGGGA	GAATCAGATG	GCATCGTTAT	ATGACGAATT	GCAAAAAGAT	TACGTAGGTC	CGGAACCACT	AGATTCCGGT	GCCGGTAACG	ATTCCAGTTT
110	120	130	140	150	160	170	180	190	200
TATACATCT	GATCATTCTC	TATCTCTATT	AAGGATATTT	CTAGTCTAAA	GTTCAAAATG	TCAAGTGTTC	TAAAGACATT	TGAAAGATTT	ACTATACAAC
210	220	230	240	250	260	270	280	290	300
AGGAGCTTCA	GGAGCAATCT	GATGACACTC	CAGTACCTCT	TGAGACAATC	AAACCTACAA	TCAGGGTATT	TGTCATCAAT	AATAATGATC	CTGTCGTAAG
310	320	330	340	350	360	370	380	390	400
ATCTAGACTT	TTATTCTTTA	ATCTACGAAT	CATTATGAGT	AACACTGCAG	GAGAGGGACA	TAGAGCTGGT	GCTCTCTCTA	GTCTTTTATC	ACTACCTTCT
410	420	430	440	450	460	470	480	490	500
GCAGCTATGA	GTAATCACAT	CAAATTAGCC	ATGCATTAC	CAGAAGCCAG	CATAGATAGA	GTAAGAGATA	CAGGGTTTGA	GAATAATTCA	TTCGGAGTCA
510	520	530	540	550	560	570	580	590	600
TTCCAGATGC	TCGATCAACT	ATGTCCAGAG	GAGAGGTGCT	GGCTTTTGAA	GCATTAGCTG	AGGACATTCC	TGATACCCTT	AATCACCAAA	CTCCATTTGT
610	620	630	640	650	660	670	680	690	700
AAATAATGAT	GTAGAAGATG	ACATATTTGA	TGAAACAGAG	AAATCTTTAG	ATGTTTGTCT	CAGTGTGCTT	ATGCAGGCAT	GGATAGTAAC	ATGCAAGTGT
710	720	730	740	750	760	770	780	790	800
ATGACTGTCT	CTGATCAACC	ACCAGTATCA	GTAGCAAAAG	GGATGGCTAA	ATATCAACAA	CAAGGGAGAA	TCAATGCTAG	GTATGTACTA	CAACCTGAAG
810	820	830	840	850	860	870	880	890	900
CACAAAGACT	AATTCGAAT	GCCATCCGCA	AGTCAATGGT	AGTAAGGCAT	TTCATGACTT	ATGAGCTTCA	ACTTTCACAA	TCAAGATCTT	TGCTAGCAAA
910	920	930	940	950	960	970	980	990	1000
CCGCTACTAT	GCTATGGTGG	GAGACATTGG	CAAGTACATT	GAACACAGCG	GAATGGGAGG	ATTTTCTCTA	ACACTTAAAT	ATGGACTTGG	AACAAGATGG
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
CCTACATGCG	CTCTTGACAG	ATTTTCTGGG	GAATCCAGCA	AATTAAGGCT	TCTCATGCTA	CATTATCAGA	GTCTAGGACC	CATGGCCAA	TACATGGCTC
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
TATTAGAATC	ACCAAACTG	ATGGATTTTG	TCCCATCTGA	ATATCCATTA	GTTTATAGCT	ATGCAATGGG	TATTGGAAC	GTCCCTTGATA	CAAATATGAG
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
AAATTATGCA	TACGGTAGAT	CATATTTAAA	TCCGCAATAT	TTTCAGCTAG	GAGTAGAAGC	AGCAAGGAAA	CAGCAGGGAG	CTGTTGACAA	CAGGACAGCA
1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
GAGGACCTCG	GCATGACTGC	TGCAGACAAA	GCAGACCTCA	CTGCAACCAT	ATCAAAGCTA	TCCTTGTCCT	AATTACCTAG	GGGTAGACAA	CCAATATCTG
1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
ACCCATTGTC	TGGAGCAAT	GACAGAGAAA	TGGGAGGACA	AGCAATGAT	ACACCTGTGT	ATAACTTCAA	TCCAATCAAT	ACTCGGAGGT	ATGACAACTA
1510	1520	1530	1540	1550	1560	1570	1580	1590	1600
TGACAGTGAT	GGTGAGGACA	GAATTGACAA	CGATCAAGAT	CAAGCTATCA	GAGAGAATAG	AGGAGAGCCT	GGACAACCAA	ACAACCAGAC	AAGTGACAAC
1610	1620	1630	1640	1650	1660	1670	1680	1690	1700
CAGCAGAGAT	TCAACCCCCC	CATACCGCAA	AGAATCATAG	GTATGAGCAG	TGAAGAGTTC	CAACATTCAA	TGAATCAGTA	CATCCGTGCT	ATGCATGAGC
1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
AATACAGAGG	CTCCAGGAT	GATGATGCCA	ATGATGCCAC	AGATGGGAAT	GACATTCTCT	TTGAGCTAGT	TGGAGATTTT	GATTCCCTAAC	TCTCAATGTC
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900
ATACAACCCG	ATATACACAT	CCACATCACT	CAGAGATACA	GCTGCCACTC	ACACACTCAT	CCAGACAAAT	CAAACCTAGC	TCACATCATT	CGGAACCAAT
1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
TCTCTCATAA	TTTAAGAAAA	AATCATAGGC	CCGGACGGGT	TAGAAATCCG	GTGCTTGTTT	GTGATCAGAT	AACCTCCACA	CCAGAATCAT	ACAATCATGG
2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
CCGAGGAACC	AACATACACC	ACTGAGCAAG	TTGATGAATT	AATCCATGCT	GGACTGGGAA	CAGTAGATTT	CTTCCTATCT	AGACCCATAG	ATGCTCAGTC
2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
TTCTTTAGGC	AAAGGCAGCA	TCCCACGAGG	TGTCACAGCT	GTTCTAACTA	GTGCAGCGGA	GGCAAAATCC	AAACCAGTTG	CTGCTGGTCC	AGTTAAACCC
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
AGGCGGAAGA	AAGTGATCAG	CAATACTACT	CCATACACTA	TTGCAGACAA	TATTCCACCT	GAGAAGCTAC	CGATCAACAC	TCCAATACCC	AATCCATTAC
2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
TTCCACTGCG	ACGCCCTCAC	GGAAAGATGA	CAGACATTGA	CATTGTCACT	GGGAACATTA	CAGAAGGATC	GTACAAAGGT	GTGAGCTTG	CTAAATTAGG
2410	2420	2430	2440	2450	2460	2470	2480	2490	2500
GAAGCAGACA	CTACTCACA	GGTTCACCTC	GAATGAGCCA	GTCTCCTCAG	CTGGATCCGC	CCAAGACCCC	AACTTTAAGA	GGGGGGGAGC	TAATAGAGAA
2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
AGAGCAAGAG	GCAACCATAG	GAGAGAATGG	AGTATTGCAT	GGGTCCGAGA	TCAGGTCAAA	GTCCTTCGAGT	GGTGTAAATCC	CAGGTGTGCC	CCAGTCACGG
2610	2620	2630	2640	2650	2660	2670	2680	2690	2700
CCTCAGCTCG	CAAGTTCAAC	TGCACATGCG	GATCCTGCCC	CAGCATCTGC	GGAGAATGTG	AAGGAGATCA	TTGAGCTCTT	AAAGGGACTT	GATCTTCGCC
2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
TTCAGACTGT	AGAAGGAAA	GTAGATAAAA	TTCTTGCAAC	TTCTGCAACT	ATAATCAATC	TTAAAAATGA	AATGACTAGT	CTCAAGGCGA	GTGTGCAAC
2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
TGTGGAAGGT	ATGATAACAA	CAATTAAAAAT	CATGGATCCC	AGTACACCAA	CTAATGTCCC	TGTAGAGGAG	ATCAGAAAGA	GTTTACACAA	TGTTCCAGTA

FIGURE 11A

2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
GTAAATGCGG	GTCCAACACTAG	TGGAGGCTTC	ACAGCCGAAG	GCAGTGATAT	GATTTCGAATG	GATGAACTAG	CTAGACCTAC	ACTCTCATCA	ACAAAAAGGA
3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
TCACACGAAA	GCCTGAATCC	AAGAAAGATT	TAACAGGCAT	AAAACCTAAT	TTGATGCAGC	TTGCAATGA	CTGCATCTCG	CGTCCAGATA	CCAAGACTGA
3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
GTTCGTGACT	AAGATTGAGG	CAGCAACAC	AGAATCACAG	CTTAACGAAA	TAAACGGTC	AATAATACGC	TCTGCAATAT	AAAATGAGGT	GCAGTCACAC
3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
AAGAGAGACT	CAACATGCAT	CCAATCAAGA	TCCAGACTCC	ATCCATCCAA	AAACACGCC	ACAATTGTCA	ACACCAAGAA	ACAACCACAG	CCGAACCATG
3310	3320	3330	3340	3350	3360	3370	3380	3390	3400
CTCAACCAAA	AGACCCAAAC	AACACCTCAC	ATCAATAGAA	GGCTGGACAT	GATAAATTTA	ATAAAAAAG	AAAAGAAGTT	AAGTAAATTT	TAAAGGACAC
3410	3420	3430	3440	3450	3460	3470	3480	3490	3500
AATAGAGAAA	ATCTAGGTCC	GAAAGCTTGC	CTCTCAGACA	GATCCCAAAA	TCATAGTCCA	AACCCCAAC	ACAGCAGCAG	ACATGCCTAT	AATATCATT
3510	3520	3530	3540	3550	3560	3570	3580	3590	3600
CCAGCAGATC	CAACTTCACC	CAGTCAATCC	CTTACTCCGT	TTCCAATACA	ACTTGACACC	AAAGATGGCA	AGGCAGGGAA	ACTCCTTAAA	CAGATTTCGAA
3610	3620	3630	3640	3650	3660	3670	3680	3690	3700
TTAGGTATCT	AAATGAGCCT	AATTTCTGCC	ATACACCAAT	AACTTTTATC	AATACGTATG	GATTTGTTTA	TGCTCGAGAC	ACTTCAGGGG	GCATTTCACAG
3710	3720	3730	3740	3750	3760	3770	3780	3790	3800
TGAGATCAGC	AGTGACCTAG	CTGCAGGGTC	CATAACAGCA	TGATGATGA	CGCTAGGTCC	TGGTCCAAAT	ATTCAGAAAT	CAATCTAGT	GCTAAGATCT
3810	3820	3830	3840	3850	3860	3870	3880	3890	3900
CTGAATGAAT	TCTACGTAAA	AGTCAAGAAG	ACATCAAGCC	AGAGAGAGGA	AGCAGTGTTC	GAATTAGTTA	ACATTCCAAC	TTTATTGAGA	GAACATGCTC
3910	3920	3930	3940	3950	3960	3970	3980	3990	4000
TTTGCAACG	CAAAATGTGA	GTATGCTCTG	CAGAAAAATT	CCTCAAGAAC	CCGTCAAAGC	TACAAGCTGG	ATTTGAGTAT	GTATACATAC	CAACTTTTGT
4010	4020	4030	4040	4050	4060	4070	4080	4090	4100
CTCCATTACA	TACTCACCAC	GAAATCTGAA	TTACCAAGTT	GCCAGACCTA	TCCTTAAGTT	CAGATCACGC	TTTGTGTATA	GCATTCATT	GGAATTAATC
4110	4120	4130	4140	4150	4160	4170	4180	4190	4200
CTGAGATTGC	TATGCAAAATC	TGACTCCCCC	TTGATGAAAT	CCTACAATGC	AGACAGAAAC	GGTCGGGGAT	GCCTCGCATC	AGTCTGGATC	CTTGTATGTA
4210	4220	4230	4240	4250	4260	4270	4280	4290	4300
ACATTCTGAA	AAACAAAAGC	ATCAAGCAAC	AAGGCAGAGA	ATCATATTTC	ATAGCTAAGT	GCATGAGCAT	GCAGCTGCAG	GTGTCCATTG	CAGATCTTTG
4310	4320	4330	4340	4350	4360	4370	4380	4390	4400
GGGACCAACA	ATCATAATCA	AATCATTTGG	TCACATCCCC	AAGACTGCAC	TTCTTTT	CAGCAAAGAT	GGGATTGCCT	GTCATCCATT	ACAAGATGTT
4410	4420	4430	4440	4450	4460	4470	4480	4490	4500
TCCCTAATC	TGACAAAATC	ACTGTGGTCA	GTTGGATGTG	AGATAGAATC	TGCCAAGTTG	ATACTTCAAG	AATCTGATCT	TAATGAGCTA	ATGGGCCACC
4510	4520	4530	4540	4550	4560	4570	4580	4590	4600
AGGACCTTAT	CACTGATAAG	ATTGCCATTA	GATCAGGTCA	ACGGACATTT	GAGAGGTCCA	AATTCAGCCC	ATTCAAAAAA	TATGCATCAA	TTCCAAACTT
4610	4620	4630	4640	4650	4660	4670	4680	4690	4700
GGAAGCCATC	AACTGAATGC	TCCAGCATCT	GAGAATAGAA	CCACAATCAA	GTCATACCTAC	TAGTCACTAT	ACAATAATCA	ACAATTTTAT	TCAACTGATT
4710	4720	4730	4740	4750	4760	4770	4780	4790	4800
ACCAAGATGT	TATCATAGGT	CCGAACGTAT	CAATCTAACA	AAAAAATCAA	ACGTTCCACA	ATAAATCAAC	GTTCAGGCCA	AAATATTTCAG	CCATGCATCA
4810	4820	4830	4840	4850	4860	4870	4880	4890	4900
CCTGCATCCA	ATGATAGTAT	GCATCTTTGT	TATGTACACT	GGAATTGTAG	GTTTCAGATGC	CATTGCTGGA	GATCAACTAC	TTAATATAGG	GGTCATTCAA
4910	4920	4930	4940	4950	4960	4970	4980	4990	5000
TCAAAGATAA	GATCACTCAT	GTACTATACT	GATGGTGGTG	CTAGCTTTAT	TGTTGTAAAA	TTGCTACCTA	ATCTTCCCCC	AAGCAATGGA	ACATGCAACA
5010	5020	5030	5040	5050	5060	5070	5080	5090	5100
TCACCACTCT	AGATGCATAT	AATGTTACCC	TATTTAAGTT	ACTAACACCC	CTGATTGAGA	ACCTGAGTAA	AATTTCCACT	GTTACAGATA	CCAAAACCCG
5110	5120	5130	5140	5150	5160	5170	5180	5190	5200
CCAAGAACGA	TTTGCAGGAG	TAGTTGTGG	ACTTGCTGCA	TTAGGAGTAG	CCACAGCCGC	ACAAATAACT	GCAGCTGTAG	CAATAGTGAA	AGCTAATGCA
5210	5220	5230	5240	5250	5260	5270	5280	5290	5300
AATGCTGCTG	CGATAAACAA	TCTTGCATCT	TCAATTCAAT	CCACCAACAA	GGCAGTATCC	GATGTGATAG	ATGCATCAAG	AACAATTGCA	ACCGCAGTTC
5310	5320	5330	5340	5350	5360	5370	5380	5390	5400
AAGCAATTCA	GGATCACATC	AATGGAGCTA	TTGTTAATGG	GATAACATCT	GCATCATGCC	GTGCCCATGA	TGCACTCATT	GGGTCAATAT	TAAATCTTTA
5410	5420	5430	5440	5450	5460	5470	5480	5490	5500
TCTCACTGAG	CTTACCACAA	TATTTCAATA	TCAAATAACA	AACCTGCGC	TGACACCACT	CTCATCCAA	GCTTTAAGAA	TCTCTCTCGG	TAGCACCTTG
5510	5520	5530	5540	5550	5560	5570	5580	5590	5600
CCAATGTGCA	TTGAGTCCAA	ACTCAACACA	AACCTCAACA	CAGCAGAGCT	GCTCAGTTCC	GGACTGTAA	CTGGTCAAAAT	AATTTCCATT	TCCCCAATGT
5610	5620	5630	5640	5650	5660	5670	5680	5690	5700
ACATGCAAAAT	GCTAATTCAA	ATCAATGTTT	CGACATTTAT	AATGCAACCC	GGTGCGAAGG	TAATTGATCT	AATGCTATC	TCCGCAAAAC	ATAAATTGCA
5710	5720	5730	5740	5750	5760	5770	5780	5790	5800
AGAAGTGGTT	GTACAAGTTC	CGAATAGGAT	TCTAGAGTAT	GCAAAATGAAC	TACAAAATTA	CCGAGCCAAT	GACTGTGTCG	TGACACCGAA	CTCTGTATTT

FIGURE 11B

5810 5820 5830 5840 5850 5860 5870 5880 5890 5900
TG TAGATACA ATGAGGGTTC CCCTATCCCT GAATCACAAT ATCAATGCTT GAGGGGGAAAT CTTAATTCTT GCACCTTTTAC CCCTATTATC GGGAACTTTT
5910 5920 5930 5940 5950 5960 5970 5980 5990 6000
TTAAGCGATT CGCATTGTCT AATGGTGTGC TCTATGCCAA CTGCAAATCT TTGCTATGTA GGTGTGCCGA CCCCCCCCAT GTTGTATCCC AGGATGATAC
6010 6020 6030 6040 6050 6060 6070 6080 6090 6100
CCAAGGCATC AGCATAATTG ATATTAAGAG ATGCTCTGAG ATGATGCTTG ACACCTTTTC ATTTAGGATC ACATCTACTT TCAATGCTAC GTACGTGACA
6110 6120 6130 6140 6150 6160 6170 6180 6190 6200
GACTTCTCAA TGATTAATGC AAATATTGTA CATCTAAGTC CTCTAGATTT GTCAAATCAA ATCAATTCAA TAAACAAATC TCTTAAAGT GCTGAGGATT
6210 6220 6230 6240 6250 6260 6270 6280 6290 6300
GGATTGCAGA TAGCAACTTC TTTGCTAATC AAGCCAGGAC AGCCAGGACA CTTTATTTCAC TAAGTGCAAT AGCATTAAATA CTATCAGTGA TTACTTTGGT
6310 6320 6330 6340 6350 6360 6370 6380 6390 6400
TGTCGTGGGA TTGCTGATTG CCTACATCAT CAAGCTGGTT TCTCAAATCC ATCAATTGAC ATCGCTAGCT GCTACAAACA TGTTCCACAG GAAAAATCCT
6410 6420 6430 6440 6450 6460 6470 6480 6490 6500
GCCCTCTTTT CCAAGAATAA CCATGGAAAC ATATATGGGA TATCTTAAGA AATCTATCAC AAGTCTATAT ATGTCCACAA TTGACCCCTA AGAACCAACT
6510 6520 6530 6540 6550 6560 6570 6580 6590 6600
TCCAACGATT ATCCGTTAAA TTAAAGTATA ATAGTTTAAA AATTAACATT AAGCCTCCAG ATACCAATGA ATATGAATAT ATCTCTTAGA AAACCTGATT
6610 6620 6630 6640 6650 6660 6670 6680 6690 6700
ATTATGTGAT AGCGTAGTAC AATTTAAGAA AAAACCTAAA ATAAGCAGCA ACCCTTAAGG TGTCGTAAAG TCTCGTGACA CCGGTTTCAG TTCAATATAC
6710 6720 6730 6740 6750 6760 6770 6780 6790 6800
GACCTCTAAC CCAATTTAAC ACCCATCTCT ATATAAGAAC ACAGTATAAT TTAATCACA AAGACCTCAA AAATGACAC AGCTTGATCC ACTCAACATA
6810 6820 6830 6840 6850 6860 6870 6880 6890 6900
TAATTGTAAG ATTAATAATA ATGGAAGATT ACAGCAATCT ATCTCTTAAA TCAATTCTCA AAAGGACATG TAGAATCATT TTCCGAAGTG CCACAATTCT
6910 6920 6930 6940 6950 6960 6970 6980 6990 7000
TGGAATATGC ACATTGATTG TTCTATGTTC AAGTATTCTT CATGAGATAA TTCATCTTGA TGTTCTCTCT GGTCTCATGG ATTCCGATGA TTCACAGCAA
7010 7020 7030 7040 7050 7060 7070 7080 7090 7100
GGCATTATTC AGCCTATTAT AGAATCATTA AAATCATTA TTGCTTTGGC TAACCAGATT CTGTACAATG TTGCAATAAT AATTCCTCTT AAAATTGACA
7110 7120 7130 7140 7150 7160 7170 7180 7190 7200
GTATCGAGAC TGTAATATAC TCTGCTTTAA AGGATATGCA TACTGGGAGC ATGTCCCAACA CCAACTGTAC ACCCGGAAAT CTGCTTCTGC ATGATGCAGC
7210 7220 7230 7240 7250 7260 7270 7280 7290 7300
GTACATCAAT GGAATAAACA AATTCCCTGT ACTTAAATCA TACAATGGGA CGCCTAAATA TGGACCTCTC CTAAATATTC CCAGCTTTAT CCCCTCAGCA
7310 7320 7330 7340 7350 7360 7370 7380 7390 7400
ACATCTCCCA ACGGGTGCAC TAGAATACCA TCATTTTCAC TCATTAAGAC CCATTGGTGT TACACTCACA ATGTAATACT TGGAGATTGC CTCGATTTC
7410 7420 7430 7440 7450 7460 7470 7480 7490 7500
CGACATCTAA TCAGTATTTA GCAATGGGGA TAATACAACA ATCTGCTGCA GCATTTCCTCA TCTTCAGGAC TATGAAAACC ATTTACCTAA GTGATGGAAT
7510 7520 7530 7540 7550 7560 7570 7580 7590 7600
CAATCGCAAA AGCTGTTTCA TCACTGCTAT ACCAGGAGGT TGTGCTTGT ATTGCTATGT AGCTACAAGA TCTGAGAAAG AAGATTATGC CACAACATGAT
7610 7620 7630 7640 7650 7660 7670 7680 7690 7700
CTAGCTGAAC TGAGACTTGC TTTCTATTAT TATAATGATA CCTTTATTGA AAGAGTCATA TCTCTTCCAA ATACAACAGG GCAATGGGCC ACAATCAATC
7710 7720 7730 7740 7750 7760 7770 7780 7790 7800
CTGCACTGG AAGCGGGATC TATCATCTAG GCTTTATTTT ATTTCCCTGTA TATGGTGGTC TCATAAAGGG GACTCCTTCC TACAACAAGC AGTCCCTCAG
7810 7820 7830 7840 7850 7860 7870 7880 7890 7900
CTATTTTATC CCAAACATC CCAACATAAC CTGTGCCGGT AAATCCAGCG AACAGGCTGC AGCAGCACGG AGTTCCTATG TAATCCGTTA TCACTCAAAC
7910 7920 7930 7940 7950 7960 7970 7980 7990 8000
AGGTGATTG AGAGTGCTGT TCTTATTGCG CCATTGTCTG ACATGCACAC AGCAAGGTGT AATCTAGTTA TGTTTAACAA TTCTCAAGTC ATGATGGGTG
8010 8020 8030 8040 8050 8060 8070 8080 8090 8100
CAGAAGGTAG GCTCTATGTT ATTGACAATA ATTTGTATTA TTATCAACGT AGTTCCCTCT GGTGGGCTGC ATCGCTTTT TACAGGATCA ATACAGATT
8110 8120 8130 8140 8150 8160 8170 8180 8190 8200
TTCTAAAGGA ATTCCTCCTA TCATTGAGGC TCAATGGGTA CCGTCCCTAT AAGTTCCCCG TCCTGGAGTC ATGCCATGCA ATGCAACAAG TTTTGGCCCT
8210 8220 8230 8240 8250 8260 8270 8280 8290 8300
GCTAATTGCA TCACAGGGGT GTACGCAGAT GTGTGGCCGC TTAACGATCC AGAACCCACA TCACAAAATG CTCTGAATCC CAACATATCGA TTGCTGGAG
8310 8320 8330 8340 8350 8360 8370 8380 8390 8400
CCTTTCTCAG AATAGTGCC AACCGAACCA ATCCACATT CTACACTGCA TCAGCCAGCG CCCTACTAAA TACTACCGGA TTCAACAACA CCAATCACAA
8410 8420 8430 8440 8450 8460 8470 8480 8490 8500
AGCAGCATAT ACGTCTTCAA CCTGCTTTAA GAATACTGGA ACTCAAAAGA TTTATTGTTT GATAATAATT GAAATGGGCT CATCTCTTTT AGGGGAGTTC
8510 8520 8530 8540 8550 8560 8570 8580 8590 8600
CAAATAATAC CATTTCTAAG GGAATAATA CCTTAATACT ATTGAATGAA GACTCCAGAT TCAATAATAA TTGAAAGGCT CTCTATCTTA TGCAATAGTT
8610 8620 8630 8640 8650 8660 8670 8680 8690 8700
ATACGTTTGG GCTGTATTAG AATGTTATAG CATTCTGCTG TTTTCCCAT ATGAAGCAAT CCTCAACAC CGACTTAGGT TCAATTTTCT CATCATTAC

FIGURE 11C

8710 8720 8730 8740 8750 8760 8770 8780 8790 8800
TGTGTGAATT CAATCTTACT AAAGTTATTC CGATATTTAA GAAAAAATAA CCTTTATATA ATGTAACAAT ACTATTAAGA TTATGATATA GGCCAGAATG

8810 8820 8830 8840 8850 8860 8870 8880 8890 8900
GCGGCCTCTT CTGAGACTACT CCTTCTCTGAA GTCCACTTGA ACTCACCAAT AGTCAAACAC AAACCTCATAT ACTACTTATT ACTAGGGCAC TTCCCGCATG

8910 8920 8930 8940 8950 8960 8970 8980 8990 9000
ATCTTGACAT TTCTGAAATA AGCCCCCTTC ACAATAATGA TTGGGATCAA ATTGCCAGAG AAGAATCCAA TCTTGCTGAA CGACTTGGAG TAGCTAAATC

9010 9020 9030 9040 9050 9060 9070 9080 9090 9100
TGAATTAATT AAACGTGTGC CCGCATTTAG AGCAACTAGA TGGCGTAGTC ATGCAGCCGT CCTTATATGG CCTTCTTGTA TACCATTCTT TGTAAATTC

9110 9120 9130 9140 9150 9160 9170 9180 9190 9200
CTACCTCATT CTAAGCTTCA ACCAGTAGAA CAATGGTACA AGTTGATCAA TGCTTCATGT AATACTATAT CTGACTCAAT TGATAGATGT ATGGAGAATA

9210 9220 9230 9240 9250 9260 9270 9280 9290 9300
TTTCTATTAA GCTTACTGGG AAAACAATC TATTCTCTCG ATCCAGAGGA ACTGCAGGTG CAGGTAAAAA CAGTAAAAAT ACCCTCAATG ATATCCAATC

9310 9320 9330 9340 9350 9360 9370 9380 9390 9400
TATTTGGGAA TCAAAACAAGT GGCAACCTAA TGTATCTTTA TGGCTTACAA TTAATATACCA AATGCGACAA CTTATAATGC ATCAAAGTTC TCGTCAGCCG

9410 9420 9430 9440 9450 9460 9470 9480 9490 9500
ACTGATTTAG TTCACATTGT TGACACACGA TCTGGTCTAA TAGTTATCAC CCCTGAACCT GTTATTGTTT TTGATCGGTT AAATAGTGT TTAATGTATT

9510 9520 9530 9540 9550 9560 9570 9580 9590 9600
TTACATTGA GATGACTTTA ATGGTAAGTG ACATGTTTGA GGGAAGGATG AATGTCACCG CTCTCTGCAC TATTAGTCAT TACTTATCTC CACTAGGGCC

9610 9620 9630 9640 9650 9660 9670 9680 9690 9700
AAGGATAGAT AGATTGTTTT CCATTGTAGA TGAATTAGCA CAACTATTAG GTGACACTGT ATATAAAGTT ATTGCATCTC TTGAATCTTT AGTATATGGG

9710 9720 9730 9740 9750 9760 9770 9780 9790 9800
TGCTTACAAC TTAAAGATCC AGTAGTGGAA TTAGCAGGGT CATTTCATTC CTTTATTACA CAAGAGATTA TAGATATCCT AATTGGTTCA AAAGCCCTTG

9810 9820 9830 9840 9850 9860 9870 9880 9890 9900
ATAAGGATGA ATCAATAACT GTTACTACAC AATTGTTAGA TATATTTTCC AACCTTCTC CAGATTTAAT TGCTGAGATG TTGTGTCTCA TGAGACTTTG

9910 9920 9930 9940 9950 9960 9970 9980 9990 10000
GGGTCAATCC ACTCTTACTG CTGCGCAAGC TGCAGGTAAA GTGAGAGAAT CTATGTGTGC AGGTAAAGTTA CTTGATTTC CTACAATAAT GAAACCTCTT

10010 10020 10030 10040 10050 10060 10070 10080 10090 10100
GCTTTTTTCC ACACAATTTT AATTAATGGT TACCGTAGAA AGAAAAATGG AATGTGGCCT CCACCTTATC TTCCTAAAAA TGCATCAAAA AGCTTAATAG

10110 10120 10130 10140 10150 10160 10170 10180 10190 10200
AATTTCACAA TGATAATGCT GAAATATCTT ACGAATATAC ACTCAAGCAT TGGAAGAGA TCTCTCTCAT AGAATTTAGA AAGTGCTTTG ACTTTGATCC

10210 10220 10230 10240 10250 10260 10270 10280 10290 10300
TGGTGAGGAG CTAAGCATT TTAGAAGA CAAGGCAATA AGTGCTCCAA GAAGTGATTG GATGAGTGTA TTTCTGTAGAA GTCTAATAAA ACAACGACAT

10310 10320 10330 10340 10350 10360 10370 10380 10390 10400
CAGAGACATC ATATTCCTAT GCCCAATCCA TTTAATAGAC GTCTATTACT CAATTCTCTA GAAGATGACA GTTTTGATCC AGTTGCCGAG CTTCAATATG

10410 10420 10430 10440 10450 10460 10470 10480 10490 10500
TTACCAGTGG TGAATATCTC CAAGATGACA CATTTTGTC ATCTTACTCA TTAAAGAGA AAGAAATAAA ACCAGATGGA AGGATATTTG CTAAGCTTAC

10510 10520 10530 10540 10550 10560 10570 10580 10590 10600
TAATAGAATG CGGTCTGTCT AAGTAATTGC GGAAGCAATT CTCGCAATC ATGCAGGTAC TCTAATGAAG GAAAACGGAG TTGTCTTGAA TCAATTATCA

10610 10620 10630 10640 10650 10660 10670 10680 10690 10700
CTGACTAAAT CATTGCTTAC TATGAGTCAA ATTTGGCATA TATCAGAAAA GGCGAAGAGA TATACGCGAG ATAACATCTC ATCCCAAGGT TTCCATACAA

10710 10720 10730 10740 10750 10760 10770 10780 10790 10800
TCAAGACTGA TTCTAAAAAT AAGAGGAAAA GCAAACTGC ATCATCATAC CTCACAGATC CTGATGATAC ATTTGAACTT AGTGCATGTT TTATAACTAC

10810 10820 10830 10840 10850 10860 10870 10880 10890 10900
TGATCTTGCT AAATACTGTC TTCAATGGAG ATATCAGACC ATAATCCATT TTGCTCGAAC ATTAAACAGA ATGTATGGAG TTCCACATTT ATTTGAATGG

10910 10920 10930 10940 10950 10960 10970 10980 10990 11000
ATTCACTTTC GTTTAATTAG ATCTACATTA TATGTTGGTG ATCCATTCAA TCCTCTGCC GCAACTGATG CTTTCGATCT AGATAAAGTA TTAATGTTG

11010 11020 11030 11040 11050 11060 11070 11080 11090 11100
ATATCTTTAT AGTCTCTCCC AAGGGAGGTA TTGAAGGCCT ATGTCAGAAA ATGTGGACAA TGATCTCTAT TTCTGTGATC ATCCTCTCTT CAGCCGAATC

11110 11120 11130 11140 11150 11160 11170 11180 11190 11200
CAAAACAAGA GTAATGAGCA TGGTTCAAGG AGATAATCAG GCGATTGCG TTAACAACAG AGTTCCTAGA TCATTACCTA GTATTGAGAA AAAGGAGTTA

11210 11220 11230 11240 11250 11260 11270 11280 11290 11300
GCCTATGCG CAAGCAAGTT ATTTTGTGAA AGACTTAGGG CAAATAATTA TGGGTGTTGGT CATCAGCTAA AGGCTCAAGA AACTATAATA AGTTCCACGT

11310 11320 11330 11340 11350 11360 11370 11380 11390 11400
TCTTCATATA TAGTAAACGG GTATTTTATC AAGGACGTAT ACTAACACAG GCACTCAAAA ATGCTAGCAA GTTATGCTTT ACTGCAGATG TATTAGGTGA

11410 11420 11430 11440 11450 11460 11470 11480 11490 11500
ATGTACTCAA GCTTCTGTG CAAATTCGCT TACTACCATC ATGAGATTAA CAGAAAATGG GGTGAGAAA GATACATGTT ATAAGCTTAA TATTATCAG

11510 11520 11530 11540 11550 11560 11570 11580 11590 11600
TCCATTCGTC AACTCACATA TGATCTAATA TTTCCCAAT ACTCCATACC AGGTGAACT ATAAGTGA TTTTCTTACA GCATCCAAGA CTAATCTCAC

FIGURE 11D

11610 11620 11630 11640 11650 11660 11670 11680 11690 11700
GTATTGTTCT GCTCCCTTCA CAGCTAGGTG GTCCTTAATTA CCTCGCATGT AGCAGATTAT TTAACCCGAA TATCGGAGAT CCTCTTGGA CAGCTGTGGC
11710 11720 11730 11740 11750 11760 11770 11780 11790 11800
AGATCTCAAG AGGTTAATTA AATGTGGTGC TCTTGAATCA TGGATACTGT ATAATTTACT AGCAAGAAAA CCAGGGAAAG GTTCATGGGC AACTTTAGCA
11810 11820 11830 11840 11850 11860 11870 11880 11890 11900
GCCGATCCAT ACTCATTGAA TCAAGAATAT CTTTATCCTC CTACTACTAT ACTTAAAGA CATACTCAA ATACTTTAAT GGAGATATGT CGGAATCCTA
11910 11920 11930 11940 11950 11960 11970 11980 11990 12000
TGTTAAAGG AGTTTTTACA GATAATGCAA AAGAGGAGGA AAATCTCCTT GCAAATTTTC TTCTTGATCG TGATATAGTA TTGCCAAGAG TTGCACACAT
12010 12020 12030 12040 12050 12060 12070 12080 12090 12100
TATAATAGAT CAATCTAGCA TCGGAAGGAA GAAACAGATA CAAGGATTTT TTGACACCAC AAGGACCATA ATGAGACGAT CATTTGAAAT CAAACCACCT
12110 12120 12130 12140 12150 12160 12170 12180 12190 12200
TCAACTAAGA AGACTCTTTC AGTCATAGAA TATAATACTA ATTACTTATC TTATAACTAC CCTGTCATAC TTAATCCTTT ACCTATTCTT GGATATTATA
12210 12220 12230 12240 12250 12260 12270 12280 12290 12300
ATTATATTAC TGACCAAACT TGCAGTATTG ATATATCTAG AAGTTTAAGA AAATTATCAT GGTCTTCTTT ATTGAATGGA AGAATCTTAG AAGGATTAGA
12310 12320 12330 12340 12350 12360 12370 12380 12390 12400
AACTCCAGAT CCAATTGAAG TTGTCAATGG TTCCTTGATT GTAGGTACAG GAGATTGTGA TTTTGTATG CAGGGTGACG ACAAATTTAC TTGGTTCTTT
12410 12420 12430 12440 12450 12460 12470 12480 12490 12500
TTACCTATGG GGATAATTAT TGATGGAAT CCTGAACTA ATCCACCCAT CAGAGTTCCA TACATTGGGT CTAGAACAGA GGAAGAAGA GTTGCATCAA
12510 12520 12530 12540 12550 12560 12570 12580 12590 12600
TGGCATATAT TAAAGGTGCC ACACACAGTT TGAAGGCTGC TCTTAGAGGC GCAGGGGTAT ATATTTGGGC ATTCGGGGAT ACTGTAGTGA ACTGGAATGA
12610 12620 12630 12640 12650 12660 12670 12680 12690 12700
TGCACCTGAT ATCGCAATA CTAGGGTTAA GATATCCCTA GAGCAACTTC AGACCCCTAC ACCTCTCTCT ACATCTGCAA ACATTACACA CCGTTTAGAT
12710 12720 12730 12740 12750 12760 12770 12780 12790 12800
GATGGAGCCA CAACACTTAA ATTCACCTCA GCTAGTTCCT ATGCATTTTC TAGTTATACT CATATATCAA ATGATCAACA ATATTAGAA ATAGATCAGA
12810 12820 12830 12840 12850 12860 12870 12880 12890 12900
GAGTAGTCGA TTCTAATATT ATTTATCAAC AATTAATGAT AACAGGACTT GGGATTATTG AGACCTACCA TAACCCACCT ATAAGGACTT CTACACAAGA
12910 12920 12930 12940 12950 12960 12970 12980 12990 13000
AATCACTCTC CATTTCGACA CTAGCTCATC TTGTTGTGTT AGAAGTGTAG ATGGTTGCCT TATATGTGAG AGCAATGGAG AGGTTCCCTCA GATCACTGTT
13010 13020 13030 13040 13050 13060 13070 13080 13090 13100
CCCTATACTA ATACATTTGT ATATGATCCT GATCCACTAG CAGATTATGA GATTGCACAC CTAGATTATC TCTCCTACCA AGCTAAAATT GGAAGTACAG
13110 13120 13130 13140 13150 13160 13170 13180 13190 13200
ATTACTACTC ACTCACTGAT AAAATTGACC TATTAGCACA TTTAACTGCA AAACAAATGA TAAACTCAAT AATTGGGTTA GATGAAACAG TATCAATTGT
13210 13220 13230 13240 13250 13260 13270 13280 13290 13300
CAATGATGCG GTTATCCTAT CTGACTATAC TAATAACTGG ATTAGTGAAT GTTCTTATAC TAAGATAGAT TTAGTTTTTA AATTAATGGC ATGGAATTTT
13310 13320 13330 13340 13350 13360 13370 13380 13390 13400
CTTCTTGAGC TTGCATTCCA GATGTACTAC TTAAGGATAT CATCTTGGAC AAATATATTT GACTATACTT ATATGACTTT ACGCAGGATA CCCGGAACCTG
13410 13420 13430 13440 13450 13460 13470 13480 13490 13500
CTCTAAATAA TATTGCAGCT ACTATTAGCC ATCCAAAATT ATTAAGACGT GCAATGAATC TTGATATTAT CACTCCTATA CATGCACCGT ATTTAGCTTC
13510 13520 13530 13540 13550 13560 13570 13580 13590 13600
ATTAGATTAT GTCAAATTAA GTATTGATGC AATTCAGTGG GGAGTTAAAC AAGTTCCTGC TGATTATCA AATGGAATG ATCTTGAAAT CTTGATTCTT
13610 13620 13630 13640 13650 13660 13670 13680 13690 13700
TCAGAGGATT CAATGGAAT TAGTGATAGG GCAATGAATC TCATTGCTAG AAACTAATC CTCCTTGAC TGTGTTAAAG TGAGAATCT ACTTTTCCAA
13710 13720 13730 13740 13750 13760 13770 13780 13790 13800
AAATTAAAGG GATGCCACCA GAAGAAAAGT GTTTAGTCTT AACTGAATAT CTAGCAATGT GTTATCAAAA TACTCATCAC TTAGATCCAG ATCTTCAAAA
13810 13820 13830 13840 13850 13860 13870 13880 13890 13900
GTATTATAT AATCTAATA ATCCAAAATT GACTGCATTT CCCAGTAACA ACTTCTACTT AACTAGAAAA ATCCTTAATC AAATTAGAGA ATCAGACGAA
13910 13920 13930 13940 13950 13960 13970 13980 13990 14000
GGACAATATA TTATCACCTC ATATTATGAA TCCTTCGAAC AATTAGAAAC AGATATAATT CTTCACCTCA CTTTAACTGC TCCTTATGAT AATTACAGAA
14010 14020 14030 14040 14050 14060 14070 14080 14090 14100
CTCTAACAAA GTTCGATTTA TCCCTTGACA TCTTTCCACA TCCAGAATCT CTCGAGAAAT ATCCTCTTCC AGTTGATCAT GACTCTCGAT CTGCAATTTT
14110 14120 14130 14140 14150 14160 14170 14180 14190 14200
AACACTAATT CCAGGCCCTC CTCTCATCA TGTATTACGA CCACTAGGAG TGTCAATCCAC AGCTTGATAT AAAGGGATAA GTTATTGTAG ATACCTAGAA
14210 14220 14230 14240 14250 14260 14270 14280 14290 14300
ACACAAAAGA TACAGACTGG TGATCATCTT TATTTAGCCG AAGGAAGCGG TGCTTCAATG TCACTTCTAG AACTCTTATT TCCAGGAGAT ACTGTCTATT
14310 14320 14330 14340 14350 14360 14370 14380 14390 14400
ATAATAGTCT TTTTAGTAGT GGAGAGAATC CTCCACAGAG AAACATATGCC CCTCTTCCAA CTCAATTGT ACAGAGTGT CCATATAAT TGTGGCAAGC
14410 14420 14430 14440 14450 14460 14470 14480 14490 14500
TGATCTTGCT GATGATAGCA ATTTGATAAA AGATTTTGTC CCATTATGGA ATGGAACGG TGCAATTACA GACTTATCAA CAAAGGATGC AGTTGCATTC

FIGURE 11E

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14510      14520      14530      14540      14550      14560      14570      14580      14590      14600
ATAATACATA AAGTAGGAGC AGAGAAAGCA TCCCTTGTCC ATATAGATCT CGAATCAACT GCTAATATAA ATCAGCAAAC TCTGTCCAGA TCCCAGATTC

14610      14620      14630      14640      14650      14660      14670      14680      14690      14700
ATTCATTAAT TATAGCAACT ACTGTTCTTA AGAGGGGTGG GATATTAATT TATAAAACAT CATGGCTTCC GTTTCTAGG TTTAGTCAAC TAGCAAGTCT

14710      14720      14730      14740      14750      14760      14770      14780      14790      14800
ACTTTGGTGC TTCTTTGACC GGATCCATCT AATACGTAGT AGCTATTCTG ATCCTCACAG TCATGAGGTT TATCTTGAT GTAGACTTGC CGCAGATTTT

14810      14820      14830      14840      14850      14860      14870      14880      14890      14900
AGAACTATCG GTTTCAGTGC AGCTCTAGTA ACTGCTACTA CTCTTCACAA TGACGGATTC ACAACAATAC ATCCTGATGT TGTTTGTAGT TATTGGCAAC

14910      14920      14930      14940      14950      14960      14970      14980      14990      15000
ACCATCTTGA AAATGTTGGG AGAGTCGGAA AAGTAATTGA TGAGATACTT GATGGTTTAG CCACCAACTT CTTCGCAGGA GATAATGGGC TTATTCTAAG

15010      15020      15030      15040      15050      15060      15070      15080      15090      15100
ATGTGGAGGA ACTCCAGCT CCAGAAAATG GTTAGAGATT GACCAGTTAG CATCATTTGA TTTGGTTCAA GATGCTCTGG TTACACTTAT CACTATACAC

15110      15120      15130      15140      15150      15160      15170      15180      15190      15200
CTAAAGGAAA TTATAGAAGT GCAGTCATCA CATAACAGAGG ATTATACATC TCTCCTCTTC ACACCTTATA ATATTGGTGC AGCAGGGAAA GTCAGAACTA

15210      15220      15230      15240      15250      15260      15270      15280      15290      15300
TCATCAAATT AATTCTAGAA CGATCTTTAA TGTATACAGT CCGAAATTGG TTAGTTTTAC CCAGTTCCAT CCGGGATTCT GTACGACAAG ATTTAGAATT

15310      15320      15330      15340      15350      15360      15370      15380      15390      15400
AGGGTCATTT AGATTAATGT CTATTTTAAG TGAACAGACA TTTCTTAAAA AGACACCCAC AAAAAAATAC TTAAGTTGATC AGCTTACAAG GACATATATA

15410      15420      15430      15440      15450      15460      15470      15480      15490      15500
TCAACCTTCT TTAAGTCTCA CTCAGTCCTT CCCCTCCACC GTCCATATCA AAAACAAATA TGGAAAGCCT TAGGTAGTGT AATATATTGT TCGGAGACAG

15510      15520      15530      15540      15550      15560      15570      15580      15590      15600
TTGATATACC TCTAATTAAA GACATTCAGA TAGAAGATAT TAATGATTTT GAAGATATCG AGAGGGGTAT CGATGGCGAA GAATTATGAC AACAAATGATT

15610      15620      15630      15640      15650
ATAAGAACTC ATGATAGTTT TATTTAAGAA AAACATATTG ATTTTCCCTT TGGT

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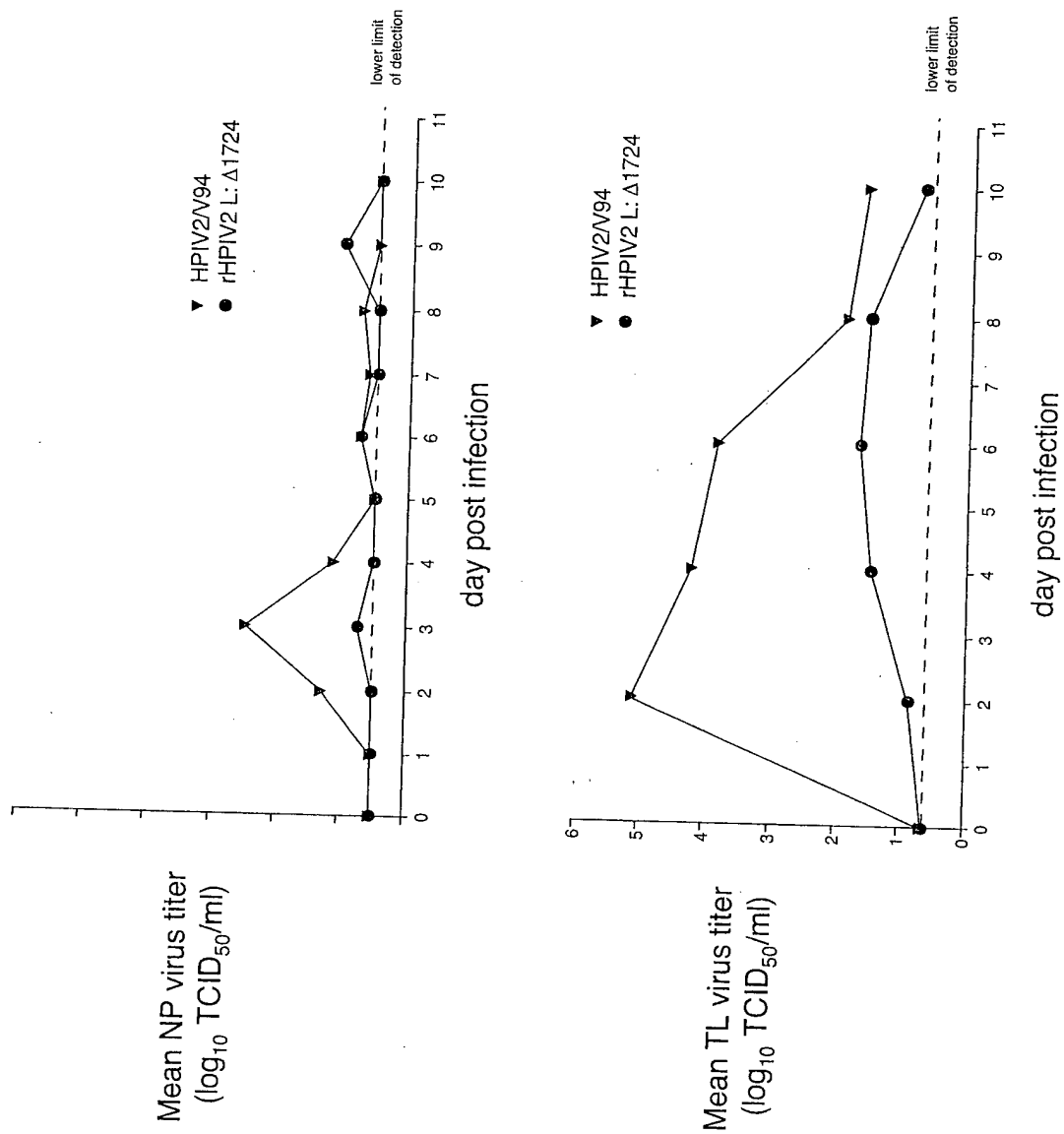


FIGURE 12

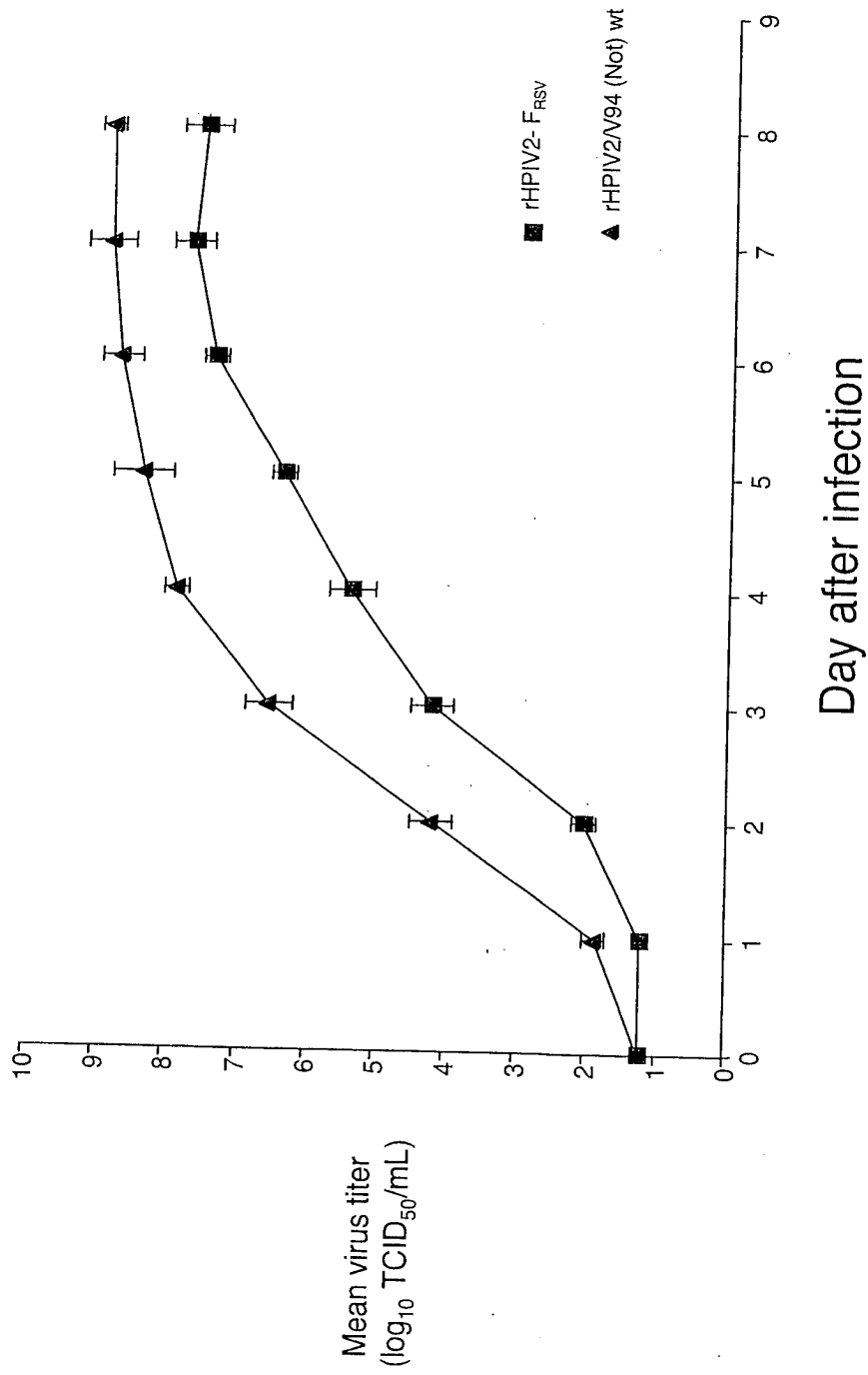


FIGURE 13

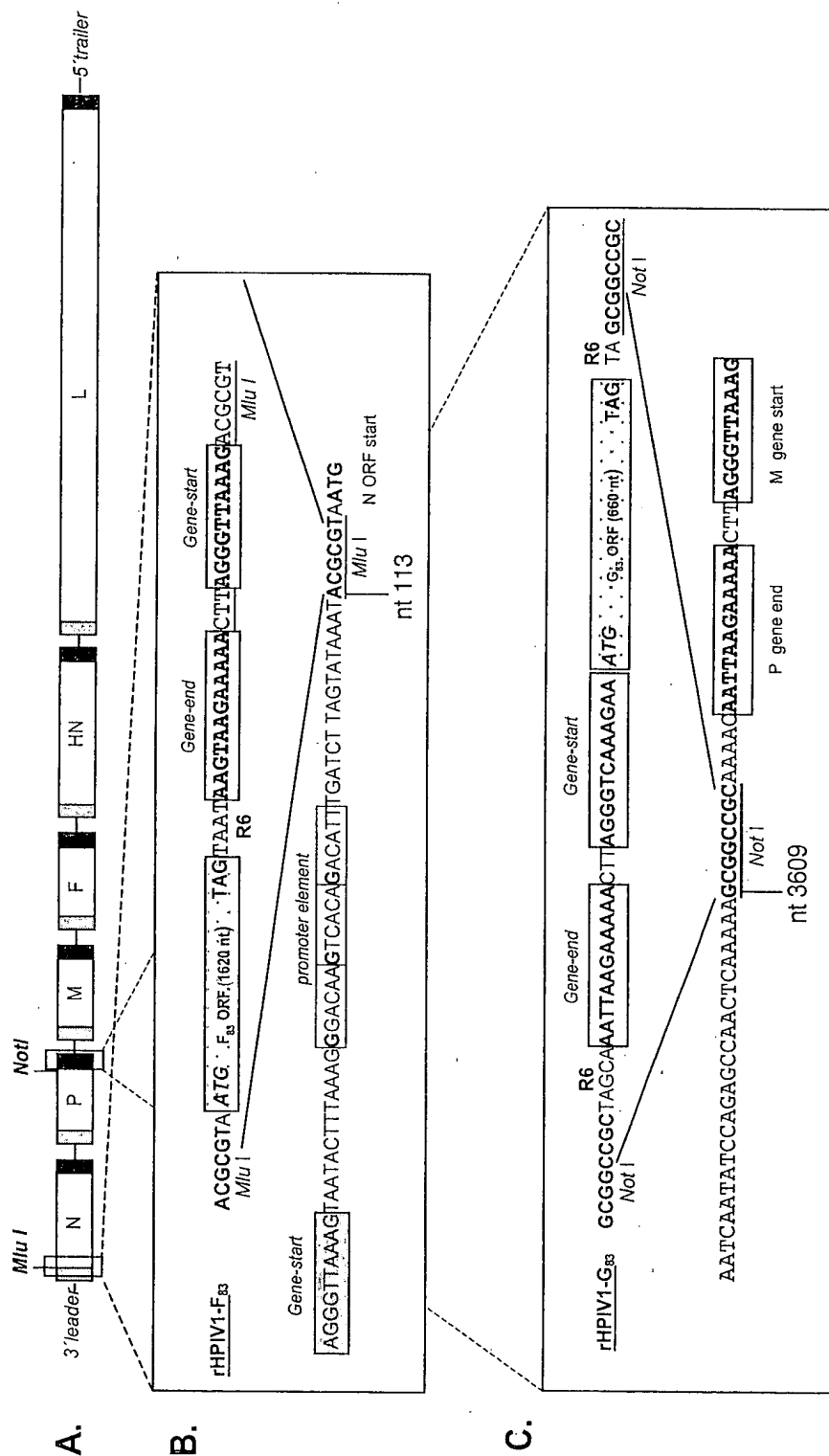


FIGURE 14